Description

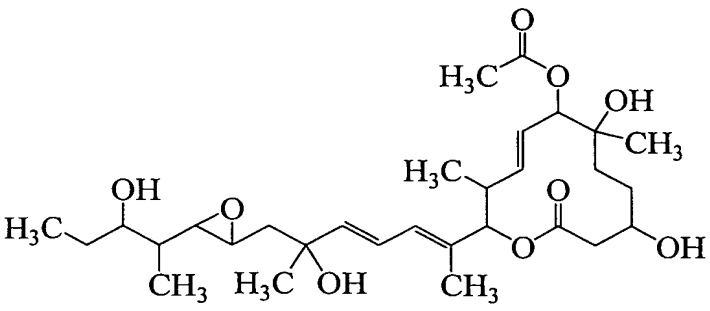
DNA participating in hydroxylation of macrolide compound

Field of the invention

The present invention relates to a DNA participating in hydroxylation of a macrolide compound, a method of isolating it, a protein encoded by the DNA, a plasmid carrying the DNA, a transformant obtained by the transformation of the plasmid and a method of producing a 16-position hydroxy macrolide compound by using the transformant.

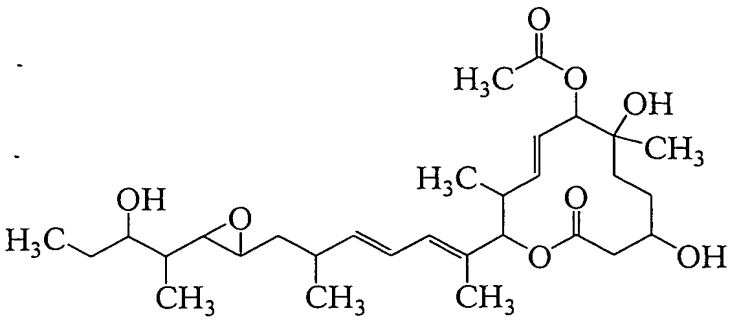
Prior Art

The 12-membered ring macrolide compound 11107D represented by the formula (II):



11107D (II)

is a 12-membered ring macrolide compound having an exellent antitumor activity and has been found, together with a 12-membered ring macrolide compound 11107B represented by the formula (I):



11107B (I),

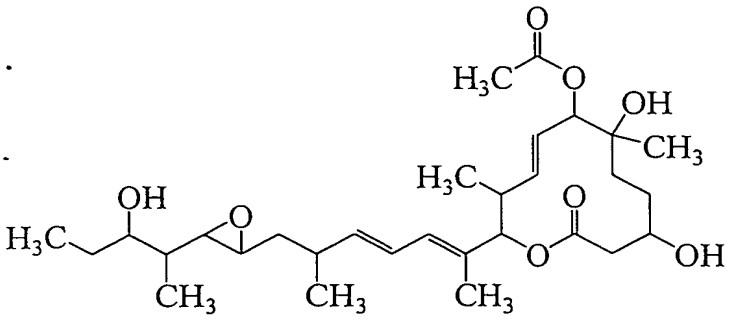
from a cultured product of a Steptmyces sp. Mer-11107 strain (WO02/060890). The macrolide compound 11107D corresponds to a 16-position hydroxylated body of the macrolide compound 11107B. The productivity of the macrolide compound 11107D is lower than that of the macrolide compound 11107B and it has been therefore desired to establish an efficient method of producing the macrolide compound 11107D.

Disclosure of the invention

The purpose of the present invention is to find a DNA participating in hydroxylation of the macrolide compound 11107B to thereby provide a novel method of producing the macrolide compound 11107D.

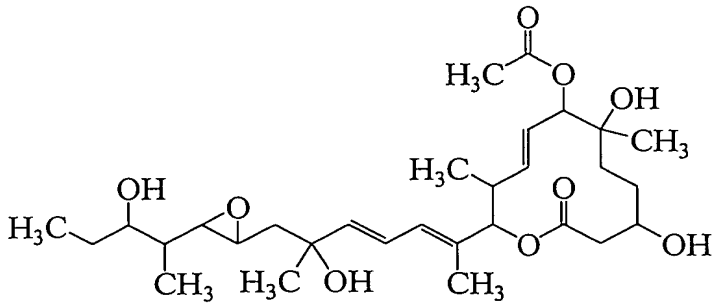
The present invention relates to the following (1) to (15):

(1) a DNA participating in biological transformation of a macrolide compound (hereinafter referred to as a macrolide compound 11107B) represented by the formula (I):



11107B (I)

into a 16-position hydroxy macrolide compound (hereinafter referred to as a macrolide compound 11107D) represented by the formula (II):



11107D (II),

the DNA being an isolated and pure DNA comprising a DNA encoding a protein having 16-position hydroxylating enzymatic activity or ferredoxin, partly or entirely or its variant;

(2) the DNA described in (1), which is characterized by the following (a), (b) or (c):

(a) a DNA encoding a protein having the enzymatic activity in hydroxylating the 16-position of the macrolide compound 11107B and selected from the group consisting of a continuous nucleotide sequence from the base 1322 to base 2548 of the sequence No. 1; a continuous nucleotide sequence from the base 420 to base 1604 of the sequence No. 2; and a continuous nucleotide sequence

from the base 172 to base 1383 of the sequence No. 3;

(b) a DNA which is a variant of the DNA described in the above (a);

(i) is hybridized with the DNA described in the above (a) under a stringent condition; and

(ii) encodes a protein having enzymatic activity in hydroxylating the 16-position of the macrolide compound 11107B; and

(c) a DNA encoding a protein having the same amino acid sequence as the protein encoded by the DNA described in the above (a) or (b) though it is not hybridized with the DNA described in the above (a) under a stringent condition because of the degeneracy of a gene codon;

(3) a protein encoded by the DNA as described in (2);

(4) a self-replicative or integrating replicative recombinant plasmid carrying the DNA as described in (2);

(5) a transformant into which the recombinant plasmid described in (4) transforms;

(6) a method of isolating a DNA encoding a protein having enzymatic activity in hydroxylating the 16-position of the macrolide compound 11107B, the method characterized by using the DNA as described in (2) or a DNA constituted of a part of the DNA as a probe or a primer;

(7) the DNA described in (1), which is characterized by the following (d), (e) or (f):

(d) a DNA encoding ferredoxin and selected from the group consisting of a continuous nucleotide sequence from the base

2564 to base 2761 of the sequence No. 1, a continuous nucleotide sequence from the base 1643 to base 1834 of the sequence No. 2 and a continuous nucleotide sequence from the base 1399 to base 1593 of the sequence No. 3;

(e) a DNA which is a variant of the DNA represented by the above (d);

(i) is hybridized with the DNA described in the above (d) under a stringent condition; and

(ii) encodes a protein having a ferredoxin function; and

(f) a DNA encoding a protein having the same amino acid sequence as the protein encoded by the DNA represented by the above (d) or (e) though it is not hybridized with the DNA described in the above (d) under a stringent condition because of the degeneracy of a gene codon;

(8) a protein encoded by the DNA as described in (7);

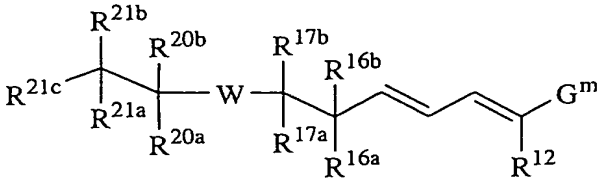
(9) a self-replicative or integrating replicative recombinant plasmid carrying the DNA as described in (7);

(10) a transformant into which the recombinant plasmid as described in (9) transforms;

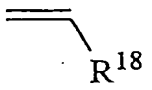
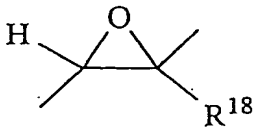
(11) a method of isolating a DNA encoding a protein having a ferredoxin function, the method characterized by using the DNA as described in (7) or a DNA constituted of a part of the DNA as a probe or a primer;

(12) a method of producing a 16-position hydroxy macrolide compound, the method comprises the steps of culturing the transformant as described in (5) or (10) in a medium; bringing

the proliferated transformant into contact with a macrolide compound represented by the formula (III):



(III)

(wherein W represents  or  ;

R^{12}, R^{16b}, R^{17a}, R^{17b}, R^{18}, R^{20a}, R^{20b}, R^{21a} and R^{21b}, which may be the same as or different from, respectively represent:

(1) hydrogen atom;

(2) a C_{1-22} alkyl group which may have a substituent;

(3) -OR (wherein R represents:

1) hydrogen atom; or

2) a C_{1-22} alkyl group;

3) a C_{7-22} aralkyl group;

4) a 5-membered to 14-membered heteroaryloxyalkyl group;

5) a C_{2-22} alkanoyl group;

6) a C_{7-15} aroyl group;

7) a C_{3-23} unsaturated alkanoyl group;

8) $-COR^{co}$ (wherein R^{co} represents:

8-1) a 5-membered to 14-membered heteroaryloxyaryl group;

8-2) a C_{1-22} alkoxy group;

8-3) an unsaturated C_{2-22} alkoxy group;

8-4) a C_{6-14} aryloxy group;

8-5) a 5-membered to 14-membered heteroaryloxy group; or

8-6) a 3-membered to 14-membered nitrogen-containing non-aromatic heterocyclic group, each of which may have a substituent);

9) a C_{1-22} alkylsulfonyl group;

10) a C_{6-14} arylsulfonyl group; or

11) $-SiR^{s1}R^{s2}R^{s3}$, (wherein R^{s1}, R^{s2} and R^{s3}, which may be the same as or different from, respectively represent a C_{1-6} alkyl group or a C_{6-14} aryl group), each of which may have a substituent);

(4) a halogen atom; or

(5) $-R^{M}-NR^{N1}R^{N2}$, {wherein R^{M} represents a single bond or -O-CO-; and R^{N1} and R^{N2}

1) may be the same as or different from, respectively represent:

1-1) hydrogen atom; or

1-2)

(i) a C_{1-22} alkyl group;

(ii) an unsaturated C_{2-22} alkyl group;

(iii) a C_{2-22} alkanoyl group;

(iv) a C_{7-15} aroyl group;

(v) an unsaturated C_{3-23} alkanoyl group;

(vi) a C_{6-14} aryl group;

(vii) a 5-membered to 14-membered heteroaryl group;

(viii) a C_{7-22} aralkyl group;

(ix) a C_{1-22} alkylsulfonyl group; or

(x) a C_{6-14} arylsulfonyl group, each of which may have a substituent, or

2) and R^{N1} and R^{N2} may be combined with the nitrogen atom to which they bound, to form a 3-membered to 14-membered nitrogen-containing non-aromatic heterocyclic group}, provided that

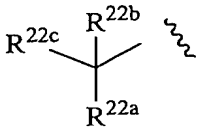
R^{21a} and R^{21b} may be combined with each other to form (i) a ketone structure (=O) or (ii) an oxime structure {=NOR^{ox} (wherein R^{ox} represents a C_{1-22} alkyl group, an unsaturated C_{2-22} alkyl group, a C_{6-14} aryl group, a 5-membered to 14-membered heteroaryl group or a C_{7-22} aralkyl group, each of which may have a substituent)};

R^{16a} represents hydrogen atom;

R^{21c} represents:

(1) hydrogen atom; or

(2)



(wherein R^{22a}, R^{22b} and R^{22c}, which may be the same as or different from, respectively represent:

1) hydrogen atom;

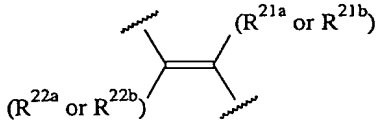
2) a C_{1-6} alkyl group;

3) -OR (wherein R has the same meaning as the above);

4) $-R^{M}-NR^{N1}R^{N2}$ (wherein R^{M}, R^{N1} and R^{N2} have the same meanings as the above); or

5) a halogen atom, or

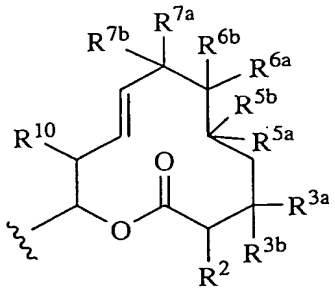
any one of R^{21a} and R^{21b} may be combined with any one of R^{22a} and R^{22b} to form the partial structure;



); and

G^m represents:

(1) a group represented by the formula (GM-I):



(GM-I)

{wherein

R^2 and R^{10}, which may be the same as or different from , respectively represent hydrogen atom or a C_{1-22} alkyl group;

R^{3a}, R^{3b}, R^{5a}, R^{5b}, R^{6a} and R^{6b}, which may be the same as or different from, respectively represent:

1) hydrogen atom;

2) hydroxyl group;

3)

3-1) a C_{1-22} alkyl group;

3-2) a C_{1-22} alkoxy group;

3-3) a C_{6-14} aryloxy group;

3-4) a 5-membered to 14-membered heteroaryloxy group;

3-5) a C_{2-22} alkanoyloxy group;

3-6) a C_{7-15} aroyloxy group;

3-7) a C_{3-23} unsaturated alkanoyloxy group;

3-8) $-OCOR^{co}$ (wherein R^{co} has the same meaning as the above);

3-9) a C_{1-22} alkylsulfonyloxy group;

3-10) a C_{6-14} arylsulfonyloxy group; or

3-11) $-OSiR^{s1}R^{s2}R^{s3}$ (wherein R^{s1}, R^{s2} and R^{s3} have the same meanings as the above), each of which may have a substituent;

4) a halogen atom; or

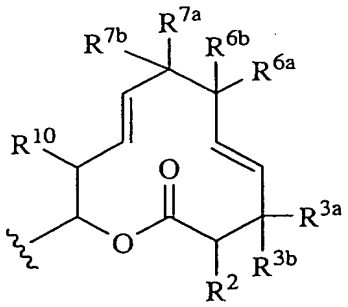
5) $-R^{M}-NR^{N1}R^{N2}$ (wherein R^{M}, R^{N1} and R^{N2} have the same meanings as the above); or

R^{5a} and R^{5b} may be combined with each other to form a ketone structure (=O); or

R^{6a} and R^{6b} may be combined with each other to form a spirooxysilanyl group or an exomethylene group; or

R^{7a} and R^{7b}, which may be the same as or different from, respectively represent hydrogen atom or $-OR^{H}$ (wherein R^{H} represents hydrogen atom, a C_{1-22} alkyl group or a C_{2-22} alkanoyl group)};

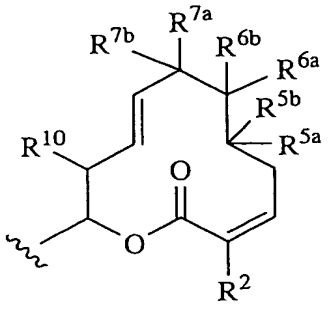
(2) a group represented by the formula (GM-II):



(GM-II)

(wherein R^2, R^{3a}, R^{3b}, R^{6a}, R^{6b}, R^{7a}, R^{7b} and R^{10} have the same meanings as those in the formula (GM-I));

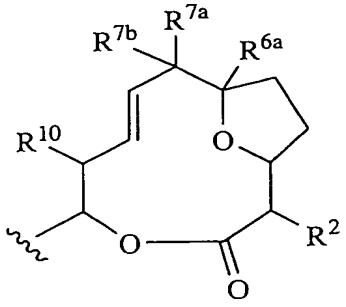
(3) a group represented by the formula (GM-III):



(GM-III)

(wherein R^2, R^{5a}, R^{5b}, R^{6a}, R^{6b}, R^{7a}, R^{7b} and R^{10} have the same meanings as those in the formula (GM-I));

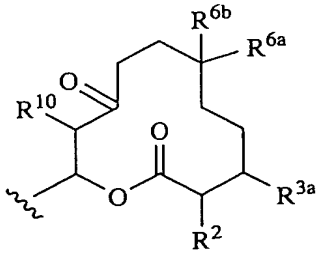
(4) a group represented by the formula (GM-IV):



(GM-IV)

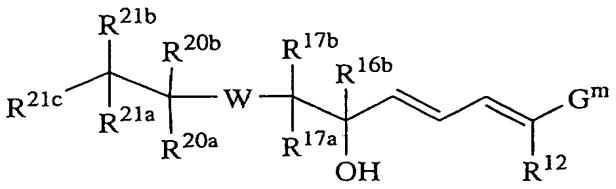
(wherein R^2, R^{6a}, R^{7a}, R^{7b} and R^{10} have the same meanings as those in the formula (GM-I)); or

(5) a group represented by the formula (GM-V):



(GM-V)

(wherein R^2, R^{3a}, R^{6a}, R^{6b} and R^{10} have the same meanings as those in the formula (GM-I))) during or after culturing, to convert it into a 16-position hydroxy macrolide compound represented by the formula (IV):

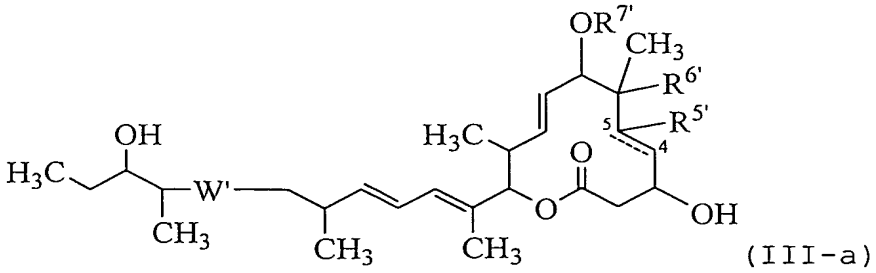


(IV)

(wherein W, R^{12}, R^{16b}, R^{17a}, R^{17b}, R^{20a}, R^{20b}, R^{21a}, R^{21b}, R^{21c} and G^m have the same meanings as those in the formula (III)); and then collecting the 16-position hydroxy macrolide compound thus converted;

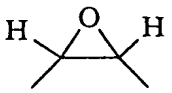
(13) a production method according to (12), wherein the transformant is the transformant as described in (5) and has a DNA encoding ferredoxin;

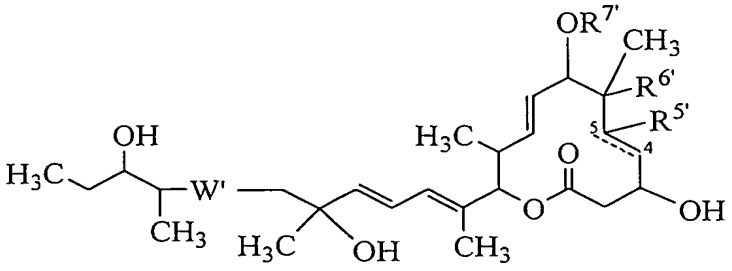
(14) the production method as described in (12), the method comprises the step of converting a compound represented by the formula (III-a):



(III-a)

(wherein $5\overset{\cdots}{=}4$ represents a double bond or a single bond; W'

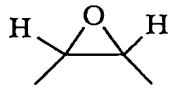
represents a double bond or  ; $R^{5'}$ represents hydrogen atom or an acetoxy group; $R^{6'}$ represents hydrogen atom or hydroxyl group; and $R^{7'}$ represents hydrogen atom or acetyl group) into a compound represented by the formula (IV-a):

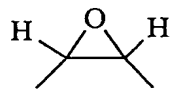


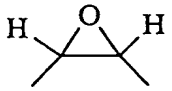
(IV-a)

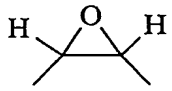
(wherein $5\overset{\cdots}{=}4$, W', $R^{5'}$, $R^{6'}$ and $R^{7'}$ have the same meanings as those in the formula (III-a));

(15) the production method as described in (14), wherein, in the conversion of the compound of the formula (III-a) into the compound of the formula (IV-a), the compound to be subjected is a compound selected from the group consisting of:

(1) a compound in which $5\overset{\cdots}{=}4$ is a single bond; W' is  ; and $R^{5'}$, $R^{6'}$ and $R^{7'}$ are respectively hydrogen atom;

(2) a compound in which $5\overset{\cdots}{=}4$ is a single bond, W' is  ; $R^{5'}$ and $R^{6'}$ are respectively hydrogen atom; and $R^{7'}$ is acetyl group;

(3) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond, W' is  ; $R^{5'}$ and $R^{7'}$ are respectively hydrogen atom; and $R^{6'}$ is hydroxyl group;

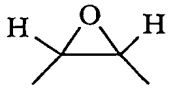
(4) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond, W' is  ; $R^{5'}$ is hydrogen atom, $R^{6'}$ is hydroxy group; and $R^{7'}$ is acetyl group;

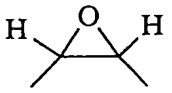
(5) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond; W' is a double bond; and $R^{5'}$, $R^{6'}$ and $R^{7'}$ are respectively hydrogen atom;

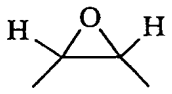
(6) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond; W' is a double bond; $R^{5'}$ and $R^{6'}$ are respectively hydrogen atom; and $R^{7'}$ is acetyl group;

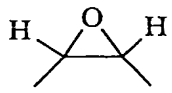
(7) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond; W' is a double bond; $R^{5'}$ and $R^{7'}$ are respectively hydrogen atom; and $R^{6'}$ is hydroxyl group;

(8) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a single bond; W' is a double bond; $R^{5'}$ is hydrogen atom; $R^{6'}$ is hydroxy group; and $R^{7'}$ is acetyl group;

(9) a compound in which $^{5}\!=\!\!-\!\!-\!^{4}$ is a double bond; W' is  ; $R^{5'}$ and $R^{7'}$ are respectively hydrogen atom; and $R^{6'}$ is hydroxyl group;

(10) a compound in which 5---4 is a double bond; W' is  ; $R^{5'}$ is hydrogen atom; $R^{6'}$ is hydroxy group; and $R^{7'}$ is acetyl group;

(11) a compound in which 5---4 is a single bond; W' is  ; $R^{5'}$ is acetoxy group; $R^{6'}$ is hydroxyl group; and $R^{7'}$ is hydrogen atom; and

(12) a compound in which 5---4 is a single bond; W' is  ; $R^{5'}$ is an acetoxy group; $R^{6'}$ is hydroxyl group; and $R^{7'}$ is acetyl group; and

(16) use of the transformant as described in (5) or (10) for producing a 16-position hydroxy macrolide compound.

The present invention made it possible to isolate a DNA encoding a protein having the enzymatic activity in hydroxylating the 16-position of a macrolide compound 11107B or ferredoxin and to determine its nucleotide sequence. Moreover, a plasmid carrying the DNA and a transformant into which the plasmid transformed were formed and a 16-position hydroxy macrolide compound could be produced using the transformant in an efficient manner.

Hereinafter, embodiments of the present invention will be explained in detail.

Microorganisms having the ability of converting a macrolide compound 11107B into a macrolide compound 11107D

In the present invention, a DNA encoding a protein having enzymatic activity in hydroxylating the 16-position or ferredoxin, partly or entirely can be isolated from the mycelia isolated from a culture broth in which microorganisms having the ability of converting the macrolide compound 11107B into the macrolide compound 11107D are cultured and the nucleotide sequence of the DNA can be determined. Then, a self-replicative or integrating replicative recombinant plasmid carrying the DNA is architecturally formed and a transformant is prepared using the plasmid.

The transformant thus prepared is cultured in the culture media and the proliferated transformant is brought into contact with the macrolide compound represented by the above formula (III) during or after culturing, to thereby covert the macrolide compound into the 16-position hydroxy macrolide compound represented by the formula (IV) and the converted 16-position hydroxy macrolide compound is collected, whereby the 16-position hydroxy macrolide compound can be obtained.

Any microorganisms having the ability of converting the macrolide compound 11107B into the macrolide compound 11107D may be used irrespective of the type of species and strain. Preferable examples of the microorganisms may include a Streptomyces sp. Mer-11107 or A-1544 strain and an unidentified Actinomyces A-1560 strain which were each isolated from soils.

It is to be noted that the Streptmyces sp. Mer-11107 was deposited as FERM P-18144 at the National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology (1-3, Higashi 1-chome Tsukuba-shi, Ibaraki-ken 305-8566 Japan) as of December 19, 2000, and then transferred to International Deposit FERM BP-7812 at International Patent Organism Depositary (IPOD) National Institute of Advanced Industrial Science and Technology (Tsukuba Central 6, 1-1, Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken 305-8566 Japan) as of November 27, 2001. The A-1544 strain was deposited as **FERM P-18943** at International Patent Organism Depositary National Institute of Advanced Industrial Science and Technology (Tsukuba Central 6, 1-1, Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken 305-8566 Japan) as of July 23, 2002, and then transferred to International Deposit FERM BP-8446 as of July 30, 2003, at International Patent Organism Depositary (IPOD) National Institute of Advanced Industrial Science and Technology (Tsukuba Central 6, 1-1, Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken 305-8566 Japan). The A-1560 strain was deposited as FERM P-19585 at the National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology (1-3, Higashi 1-chome Tsukuba-shi, Ibaraki-ken 305-8566 Japan) as of November 13, 2003 and then transferred to International Deposit FERM BP-10102 as of August 19, 2004, at International Patent Organism Depositary (IPOD) National Institute of Advanced Industrial Science and Technology (Tsukuba Central 6, 1-1, Higashi 1-Chome, Tsukuba-shi, Ibaraki-ken 305-8566 Japan).

The taxonomical properties of the above strains are as follows.

(Taxonomical properties of the Mer-11107 strain)

(1) Morphological characteristics

Spiriles type aerial hyphae were extended from the vegetative hyphae. Spore chains consisting of about 10 to 20 cylindrical spores were formed at the end of the matured aerial hyphae. The size of the spores was about 0.7 × 1.0 μm, the surface of the spores was smooth, and specific organs such as sporangium, sclerotium and flagellum were not observed.

(2) Cultural characteristics on various media

Cultural characteristics of the strain after incubation at 28°C for two weeks on various media are shown as follows. The color tone is described by the color names and codes which are shown in the parentheses of Tresner's Color wheels.

1) Yeast extract-malt extract agar medium

The strain grew well, the aerial hyphae grew up on the surface, and light gray spores (Light gray; d) were observed. The reverse side of colony was Light melon yellow (3ea). Soluble pigment was not produced.

2) Oatmeal agar medium

The strain grew moderately, the aerial hyphae grew slightly on the surface, and gray spores (Gray; g) were observed. The reverse side of colony was Nude tan (4gc) or Putty (1 1/2ec). Soluble pigment was not produced.

3) Inorganic salts-starch agar medium

The strain grew well, the aerial hyphae grew up on the surface, and gray spores (Gray; e) were observed. The reverse side of colony was Fawn (4ig) or Gray (g). Soluble pigment was not produced.

4) Glycerol-asparagine agar medium

The strain grew well, the aerial hyphae grew up on the surface, and white spores (White; a) were observed. The reverse side of colony was Pearl pink (3ca). Soluble pigment was not produced.

5) Peptone-yeast extract-iron agar medium

The strain growth was bad, and the aerial hyphae did not grow on the surface. The reverse side of colony was Light melon yellow (3ea). Soluble pigment was not produced.

6) Tyrosine agar medium

The strain grew well, the aerial hyphae grew up on the surface, and white spores (White; a) were observed. The reverse side of colony was Pearl pink (3ca). Soluble pigment was not produced.

(3) Utilization of various carbon sources

Various carbon sources were added to Pridham-Gottlieb agar and incubated 28°C for 2 weeks. The growth of the strain is shown below.

1) L-arabinose	±
2) D-xylose	±
3) D-glucose	+
4) D-fructose	+
5) Sucrose	+
6) Inositol	+

7) L-rhamnose -

8) D-mannitol +

9) Raffinose +

(+ positive, ± slightly positive, - negative)

(4) Various physiological properties

Various physiological properties of the present strain are as follows.

(a) Range of growth temperature (yeast extract-malt extract agar, incubation for 2 weeks): 12°C to 37°C

(b) Range of optimum growth temperature (yeast extract-malt extract agar, incubation for 2 weeks): 21°C to 33°C

(c) Liquefaction of gelatin (glucose-peptone-gelatin medium): negative

(d) Coagulation of milk (skim milk medium): negative

(e) Peptonization of milk (skim milk medium): negative

(f) Hydrolysis of starch (inorganic salts-starch agar): positive

(g) Formation of melanoid pigment (peptone-yeast extract-iron agar): negative

(tyrosine agar): negative

(h) Production of hydrogen sulfide (peptone-yeast extract-iron agar): negative

(i) Reduction of nitrate (broth containing 0.1% potassium nitrate): negative

(j) Sodium chloride tolerance (yeast extract-malt extract agar, incubation for 2 weeks): grown at a salt content of 4% or less

(5) Chemotaxonomy

LL-diaminopimelic acid and glycin were detected from the cell wall of the present strain.

(Taxonomical properties of the A-1544 strain)

(1) Morphological characteristics

Spira type aerial hyphae were extended from vegetative hyphae in this strain. Spore chains consisting of about 10 to 20 of cylindrical spores were formed at the end of the matured aerial hyphae. The size of the spores was about 1.0 × 1.2 to 1.4 μm, the surface of the spores was spiny, and specific organs such as sporangium, sclerotium and flagellum were not observed.

(2) Cultural characteristics on various media

Cultural characteristics of the strain after incubation at 28°C for two weeks on various media are shown in Table 1. The color tone is described by the color names and codes which are shown in the parentheses of Tresner's Color wheels.

Table 1

Medium	Growth	Aerial hyphae	Color of vegetative hyphae	Soluble pigment
Yeast extract - malt extract agar (ISP-2)	Good	Thick Silver gray (3fe)	Light melon yellow (3ea)	None
Oatmeal agar (ISP-3)	Good	Abundant Light gray to Silver gray (d to 3fe)	Light melon yellow (3ea)	None
Inorganic salts - starch agar (ISP-4)	Good	Abundant Silver gray (3fe)	Light melon yellow (3ea)	None
Glycerol - asparagine agar (ISP-5)	Good	Abundant Ashes (5fe)	Light melon yellow (3ea)	None
Peptone-yeast extract - iron agar (ISP-6)	Good	None	Light melon yellow (3ea)	Pale blackish brown
Tyrosine agar (ISP-7)	Good	Abundant Covert gray (2fe)	Light melon yellow (3ea)	None

(3) Utilization of various carbon sources

Various carbon sources were added to Pridham-Gottlieb agar and incubated at 28°C for 2 weeks. The growth of the strain is shown in Table 2.

Table 2

D-glucose	+	inositol	-
L-arabinose	+	L-rhamnose	+
D-xylose	+	D-mannitol	+
D-fructose	+	raffinose	-
sucrose	-		

+: positive, ±: slightly positive, -: negative

(4) Various physiological properties

Various physiological properties of the present strain are as follows.

(a) Range of growth temperature (yeast extract-malt extract agar, incubation for 2 weeks): 15°C to 41°C

(b) Range of optimum growth temperature (yeast extract-malt extract agar, incubation for 2 weeks): 20°C to 37°C

(c) Liquefaction of gelatin (glucose-peptone-gelatin medium): positive

(d) Coagulation of milk (skim milk medium): positive

(e) Peptonization of milk (skim milk medium): positive

(f) Hydrolysis of starch (inorganic salts-starch agar): positive

(g) Formation of melanoid pigment (peptone-yeast extract-iron agar): positive

(tyrosine agar): negative

(h) Production of hydrogen sulfide (peptone-yeast extract-iron agar): positive

(i) Reduction of nitrate (broth containing 0.1% potassium nitrate): negative

(j) Sodium chloride tolerance (yeast extract-malt extract agar,

incubation for 2 weeks): grown at a salt content of 7% or less

(5) Chemotaxonomy

LL-diaminopimelic acid was detected from the cell wall of the present strain.

DNA of the present invention

The present inventors have isolated a DNA participating in the hydroxylation of the 16-position of a macrolide compound, specifically, a DNA encoding a protein having 16-position hydroxylating enzymatic activity and a DNA encoding a protein having a ferredoxin function from the above microorganisms and determined the nucleotide sequence of the DNA. The DNA encoding a protein having 16-position hydroxylating enzymatic activity and the DNA encoding a protein having a ferredoxin function are hereinafter generically called "a 16-position hydroxylating enzyme relevant DNA" as the case may be.

The DNA encoding a protein having 16-position hydroxylating enzymatic activity is those represented by the following (1-1), (1-2) or (1-3):

(1-1) a DNA selected from those having a continuous nucleotide sequence from the base 1322 to base 2548 of the sequence No. 1, a continuous nucleotide sequence from the base 420 to base 1604 of the sequence No. 2 and a continuous nucleotide sequence from the base 172 to base 1383 of the sequence No. 3;

(1-2) a DNA which is a variant of the DNA described in the above (1-1);

(i) is hybridized with any one of the DNAs described in the above

(1-1) under a stringent condition; and

(ii) codes a protein having enzymatic activity in hydroxylating the 16-position of the macrolide compound; and

(1-3) a DNA encoding a protein having the same amino acid sequence as the protein encoded by the DNA described in the above (1-1) or (1-2) though it is not hybridized with any of the DNA described in the above (1-1) or (1-2) under a stringent condition because of the degeneracy of a gene codon.

The "16-position hydroxylating enzymatic activity" means such enzymatic activity as to hydroxylate the 16-position of the macrolide compound 11107B represented by the formula (I) to thereby convert the macrolide compound into the macrolide compound 11107D represented by the formula (II).

The DNA encoding a protein having a ferredoxin function in the present invention is those represented by the following (2-1), (2-2) or (2-3).

(2-1) a DNA encoding ferredoxin and selected from the group consisting of a continuous nucleotide sequence from the base 2564 to base 2761 of the sequence No. 1, a continuous nucleotide sequence from the base 1643 to base 1834 of the sequence No. 2 and a continuous nucleotide sequence from the base 1399 to base 1593 of the sequence No. 3;

(2-2) a DNA which is a variant of the DNA described in the above (2-1);

(i) is hybridized with the DNA described in the above (2-1) under a stringent condition; and

(ii) codes a protein having a ferredoxin function; and

(2-3) a DNA encoding a protein having the same amino acid sequence as the protein encoded by the DNA represented by the above (2-1) or (2-2) though it is not hybridized with the DNA represented by the above (2-1) under a stringent condition because of the degeneracy of a gene codon.

"The ferredoxin function" means the protein function of transferring electrons to the above 16-position hydroxylating enzyme to bear a role together with the above 16-position hydroxylating enzyme in the hydroxylation reaction.

Also, "the nucleotide sequence hybridized under a stringent condition" means a DNA nucleotide sequence obtained when any one of the DNAs of the above (1-1) and (1-2) is used as a probe and, for example, a colony hybridization method, plaque hybridization method or Southern blot hybridization method is used. Examples of the DNA having such a nucleotide sequence may include those identified by carrying out hybridization in the presence of 0.7 to 1.0 M NaCl at 65°C using a filter to which a DNA derived from a colony or a plaque or a fragment of the DNA is fixed and then washing the filter at 65°C by using 0.1 to 2 × SSC solution (1 × SSC solution: 150 mM sodium chloride and 15 mM sodium citrate). The hybridization may be carried out according to the method described in Molecular Cloning: A laboratory Mannual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY., 1989 (hereinafter abbreviated as molecular cloning, 2nd ed.).

Examples of the DNA hybridized in a stringent condition include DNAs having a nucleotide sequence having a certain level or more of homology with the nucleotide sequence of the DNA to be used as the probe, and specifically DNAs having a nucleotide sequence having 80% or more, preferably 85% or more, more preferably 90% or more, still more preferably 95% or more and most preferably 98% or more homology with the nucleotide sequence of the DNA used as the probe.

There is no particular limitation to a method of obtaining the 16-position hydroxylating enzyme relevant DNA. An appropriate probe or a primer is prepared based on the information of the nucleotide sequence described in the sequence No. 1, No. 2 or No. 3 of the sequence chart in this specification. Using the probe or primer, a DNA library of microorganisms belonging to Actinomyces is screened, and thus the DNA of the present invention can be isolated. The DNA library can be produced by the usual method from microorganisms expressing the aforementioned 16-position hydroxylating enzymatic activity.

The 16-position hydroxylating enzyme relevant DNA of the present invention can also be obtained by a PCR method. A DNA library derived from the aforementioned microorganisms is used as a template and a pair of primers which are so designed as to amplify any one of the nucleotide sequences described in the sequence No. 1, No. 2 or No. 3 are used to carry out PCR. The reaction condition of the PCR may be appropriately designed. Examples of the reaction condition may include the condition

of a process in which the cycle of the process involving a reaction run at 94°C for 30 seconds (denaturing), a reaction run at 55°C for 30 seconds to one minute (annealing) and a reaction run at 72°C for 2 minutes (extension) is repeated 30 times and then a reaction is run at 72°C for 7 minutes. Then, the amplified DNA fragment can be cloned in a vector which can be amplified in a proper host.

The aforementioned operations such as the preparation of a probe or a primer, the construction of a DNA library, the screening of a DNA library and the cloning of a target gene are obvious to a person skilled in the art and may be carried out according to methods as described in for example, Molecular Cloning 2nd ed., Current Protocols in Molecular Biology, Supplement 1 to 38, John Wiley & Sons (1987-1997).

No particular limitation is imposed on a method of obtaining the protein in the present invention. The protein may be a protein synthesized by chemical synthesis or a recombinant protein produced by gene recombination techniques. When the recombinant protein is produced, first, the DNA encoding the protein as described above in this specification is obtained. The protein of the present invention can be produced by introducing this DNA into a proper expression system. Manifestation of the protein in the expression system will be described later in the specification.

Recombinant vector in the present invention

The DNA of the present invention may be used in the situation

where it is inserted in an appropriate vector. No particular limitation is imposed on the kind of the vector to be used in the present invention and the vector may be either a self-repricative one (for example, a plasmid) or one that is incorporated into a genome of a host cell when introduced into the host cell and is replicated together with the incorporated chromosome. In the expression vector, the DNA of the present invention is operationally linked to elements (for example, a promoter) which are necessary for transcription. The promoter is a DNA sequence exhibiting transcriptional activity in a host cell and may be selected suitably corresponding to the type of host.

The transformant of the present invention and production of a recombinant protein using the transformant

The transformant may be produced by introducing the DNA or recombinant vector of the present invention into an appropriate host. The host cell into which the DNA or recombinant vector of the present invention is introduced may be any desired cell which can express the gene according to the present invention. Examples of the host cell include bacteria, yeast, fungi and higher eucaryotec cells. Examples of the bacterial cell include Gram-positive bacteria such as Bacillus or Streptomyces or Gram-negative bacteria such as E. coli. The transformation of these bacteria may be accomplished using a competent cell according to a protoplast method, electroporation method or other known methods. For example, the electroporation method may be

performed as follows. A plasmid into which a foreign gene is inserted is added to a suspension of the competent cell, this suspension is poured into a cuvet specially used for an electroporation method and high-voltage electric pulse is applied to the cuvet. Then, the cells are cultured in a selective medium and a transformant is isolated on a plate agar media.

Examples of the yeast cell include cells belonging to Saccharomyces or Schizosaccharomyces. Specific examples of the yeast cell include Saccharomyces cerevisiae or Saccharomyces kluyveri. Examples of a method of introducing the recombinant vector into the yeast host may include an electroporation method, spheroplasto method and lithium acetate method. Examples of the above other fungus cell include mycotic cells belonging to Aspergillus, Neurospora, Fusarium or Trichoderma. When mold fungi are used as the host cell, a DNA architecture is incorporated into a host chromosome to obtain a recombinant host cell, whereby transformation can be accomplished. The incorporation of the DNA architecture into the host chromosome can be accomplished, for example, by homologous recombination or heterologous recombination.

The above transformant is cultured in an appropriate nutrient medium under the condition enabling the expression of the introduced gene. In order to isolate the protein of the invention from the culture product of the transformant and to purify the protein, the usual protein isolating and purifying method may be used.

For example, when the protein of the present invention is expressed in a soluble form in cells, the cells are collected by centrifugation after the cultivation is finished and are suspended in a buffer solution. Then, the suspended solution is subjected to, for example, a ultrasonic crusher to break the cells, thereby obtaining a cell-free extract and the cell-free extract is centrifuged. A purified preparation can be obtained from the obtained supernatant by combining measures such as the usual isolation and purifying methods such as a solvent extraction method, salting-out method using ammonium sulfate, desalting method, precipitation method using an organic solvent, anion exchange chromatography using a resin such as diethylaminoethyl (DEAE) sepharose, cation exchange chromatography using a resin such as SP-Sepharose FF (manufactured by Amasham Bioscience Company), hydrophobic chromatography using a resin such as butyl sepharose and phenyl sepharose, gel filtration method using a molecular sieve, affinity chromatography, chromato-focusing method and electrophoresis method such as an isoelectric focusing electrophoresis.

Method of production of 16-position hydroxy macrolide compounds

The present invention involves a method of producing 16-position hydroxy macrolide compounds represented by the above formula (IV), the method comprising using a transformant into which a DNA encoding a protein having 16-position hydroxylating enzymatic activity or a protein having a ferredoxin function

is introduced and hydroxylating macrolide compounds represented by the above formula (III) in the presence of the transformant.

The macrolide compounds that can be hydroxylated by the transformant of the present invention is macrolide compounds represented by the above formula (III) (macrolide compounds represented by the above formula (IV)), preferably macrolide compounds represented by the above formula (III-a) (macrolide compounds represented by the above formula (IV-a) and more preferably the macrolide compound 11107B (macrolide compound 11107D). The compounds in the parenthesis are 16-position hydroxy macrolide compounds that are hydroxylated products.

The condition under which the macrolide compounds are hydroxylated in the presence of the transformant is as follows.

First, the 16-position hydroxylating enzyme relevant DNA in the transformant is expressed by adding, if necessary, inducing materials. The strain expressing the DNA is brought into contact with the macrolide compounds represented by the above formula (III) to run a conversion reaction. The temperature of the conversion reaction may be suitably determined taking the optimum growth temperature of the transformant into account. The reaction time may also be suitably determined in consideration of the conversion rate (degree of progress of the reaction) into the 16-position hydroxy macrolide compound. For example, the condition of 20 to 31°C and 1 to 5 days is preferable. Moreover, as to the reaction system, the reaction may be run in any system including a batch system or a continuous system.

For the isolation and purifying of the produced 16-position hydroxy macrolide compounds, the separation and purifying method used usually to isolate a microbial metabolite from the culture broth may be utilized. All known separation and purifying methods such as organic solvent extraction using methanol, ethanol, acetone, butanol, ethyl acetate, butyl acetate, chloroform or toluene, absorption chromatograph using a hydrophobic adhesive resin such as Diaion HP-20, gel filtration chromatography using Sefadex LH-20, adsorption chromatography using activated carbon, silica gel or the like, absorption chromatograph using thin-layer chromatography and high-performance liquid chromatography using an reverse phase column are equivalent to these separation and purifying methods. The separation and purifying method is not limited to these methods shown here. These methods may be used singly or in combinations of two or more in an optional order or repeatedly, which makes it possible to isolate and purify the target 16-position hydroxy macrolide compounds.

The variant of the DNA in the present invention means a DNA that is obtained by modifying the DNA by deletion, conversion, addition or insertion treatments in the structural base of the DNA or its derivatives and shows the same effects as the original DNA.

The "halogen atom" used in the specification of the present application means a fluorine atom, a chlorine atom, a bromine atom and an iodine atom.

The "C_{1-22} alkyl group" used in the specification of the present application indicates a linear or branched alkyl group having 1 to 22 carbon atoms, such as methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group, tert-butyl group, n-pentyl group, 1,1-dimethylpropyl group, 1,2-dimethylpropyl group, 2,2-dimethylpropyl group, 1-ethylpropyl group, n-hexyl group, 1-ethyl-2-methylpropyl group, 1,1,2-trimethylpropyl group, 1-methylbutyl group, 2-methylbutyl group, 1,1-dimethylbutyl group, 1,2-dimethylbutyl group, 2,2-dimethylbutyl group, 1,3-dimethylbutyl group, 2,3-dimethylbutyl group, 1-ethylbutyl group, 2-ethylbutyl group, 2-methylpentyl group, 3-methylpentyl group, n-heptyl group, n-octyl group, n-nonyl group or n-decyl group; preferably a linear or branched alkyl group having 1 to 6 carbon atoms, such as methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group or tert-butyl group.

The "unsaturated C_{2-22} alkyl group" used in the specification of the present application indicates a linear or branched alkenyl group having 2 to 22 carbon atoms or a linear or branched alkynyl group having 2 to 22 carbon atoms, such as vinyl group, allyl group, 1-propenyl group, isopropenyl group, 2-methyl-1-propenyl group, 2-methyl-2-propenyl group, 1-butenyl group, 2-butenyl group, 3-butenyl group, 1-pentenyl group, 1-hexenyl group, 1,3-hexanedienyl group, 1,5-hexanedienyl group, ethynyl group, 1-propynyl group,

2-propynyl group, 1-butynyl group, 2-butynyl group, 3-butynyl group, 1-ethynyl-2-propynyl group, 2-methyl-2-propynyl group, 1-pentynyl group, 1-hexynyl group, 1,3-hexanediynyl group or 1,5-hexanediynyl group. It preferably indicates a linear or branched alkenyl group having 2 to 10 carbon atoms or a linear or branched alkynyl group having 2 to 10 carbon atoms, such as vinyl group, allyl group, 1-propenyl group, isopropenyl group, ethynyl group, 1-propynyl group, 2-propynyl group, 1-butynyl group, 2-butynyl group or 3-butynyl group.

The "C_{6-14} aryl group" used in the specification of the present application means an aromatic hydrocarbon group having 6 to 14 carbon atoms, and a monocyclic group and condensed rings such as a bicyclic group and a tricyclic group are included. Examples thereof are phenyl group, indenyl group, 1-naphthyl group, 2-naphthyl group, azulenyl group, heptalenyl group, indacenyl group, acenaphthyl group, fluorenyl group, phenalenyl group, phenanthrenyl group and anthracenyl group; of which a preferred example is phenyl group, 1-naphthyl group or 2-naphthyl group.

The "5-membered to 14-membered heteroaryl group" used in the specification of the present application means a monocyclic, bicyclic or tricyclic 5-membered to 14-membered aromatic heterocyclic group which contains one or more of hetero atoms selected from the group consisting of a nitrogen atom, sulfur atom and oxygen atom. Preferred examples thereof are a nitrogen-containing aromatic heterocyclic group such as pyrrolyl group, pyridinyl group, pyridazinyl group, pyrimidinyl

group, pyrazinyl group, triazolyl group, tetrazolyl group, benzotriazolyl group, pyrazolyl group, imidazolyl group, benzimidazolyl group, indolyl group, isoindolyl group, indolizinyl group, purinyl group, indazolyl group, quinolinyl group, isoquinolinyl group, quinolizinyl group, phthalazinyl group, naphthyridinyl group, quinoxalinyl group, quinazolinyl group, cinnolinyl group, pteridinyl group, imidazotriazinyl group, pyrazinopyridazinyl group, acridinyl group, phenanthridinyl group, carbazolyl group, carbazolinyl group, perimidinyl group, phenanthrolinyl group, phenazinyl group, imidazopyridinyl group, imidazopyrimidinyl group, pyrazolopyridinyl group or pyrazolopyridinyl group; a sulfur-containing aromatic heterocyclic group such as thienyl group or benzothienyl group; and an oxygen-containing aromatic heterocyclic group such as furyl group, pyranyl group, cyclopentapyranyl group, benzofuryl group or isobenzofuryl group; an aromatic heterocyclic group containing two or more different hetero atoms, such as thiazolyl group, isothiazolyl group, benzothiazolyl group, benzothiadiazolyl group, phenothiazinyl group, isoxazolyl group, furazanyl group, phenoxazinyl group, oxazolyl group, isoxazoyl group, benzoxazolyl group, oxadiazolyl group, pyrazolooxazolyl group, imidazothiazolyl group, thienofuranyl group, furopyrrolyl group or pyridoxazinyl group, of which a preferred example is thienyl group, furyl group, pyridinyl group, pyridazinyl group, pyrimidinyl group or pyrazinyl group.

The "3-membered to 14-membered nitrogen-containing non-aromatic heterocyclic group" used in the specification of the present application means a monocyclic, bicyclic or tricyclic 3-membered to 14-membered non-aromatic heterocyclic group containing one or more nitrogen atoms. Preferable examples thereof include an azilidinyl group, azetizyl group, pyrrolidinyl group, pyrrolyl group, piperidinyl group, piperazinyl group, homopiperidinyl group, homopiperazinyl group, imidazolyl group, pyrazolidinyl group, imidazolidinyl, morpholinyl group, thiomorpholinyl group, imidazolinyl group, oxazolinyl group and quinuclidinyl group. The nitrogen-containing non-aromatic heterocyclic group also includes a group derived from a pyridone ring and a non-aromatic condensed ring (such as a group derived from a phthalimide ring or succinimide ring).

The "C_{2-22} alkanoyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" in which the end thereof is a carbonyl group. Examples threof include acetyl group, propionyl group, butyryl group, iso-butyryl group, valeryl group, iso-valeryl group, pivalyl group, caproyl group, decanoyl group, lauroyl group, myristoyl group, palmitoyl group, stearoyl group and arachidoyl group. Preferable examples thereof include alkanoyl groups having 2 to 6 carbon atoms such as acetyl group, propionyl group, butyryl group or iso-butyryl group.

The "C_{7-15} aroyl group" used in the specification of the

present application means a group corresponding to the above-defined "C_{6-14} aryl group" or "5-membered to 14-membered heteroaryl group" to each of which end a carbonyl group is bonded. Examples thereof include benzoyl group, 1-naphthoyl group, 2-naphthoyl group, picolinoyl group, nicotinoyl group, isonicotinoyl group and furoyl group.

The "C_{3-23} unsaturated alkanoyl group" used in the specification of the present application means a group corresponding to the above-defined "unsaturated C_{2-22} alkyl group" to which end a carbonyl group is bonded. Examples thereof include an acryloyl group, propioloyl group, crotonoyl group, iso-crotonoyl group, oleloyl group and linolenoyl group. Preferable examples thereof include unsaturated alkanoyl groups having 2 to 6 carbon atoms and specifically an acryloyl group.

The "C_{7-22} aralkyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkyl group" of which substitutable moiety is replaced by the above-defined "C_{6-14} aryl group" and being constituted of 7 to 22 carbon atoms. Specific examples thereof are benzyl group, phenethyl group, 3-phenylpropyl group, 4-phenylbutyl group, 1-naphthylmethyl group and 2-naphthylmethyl group, of which an aralkyl group having 7 to 10 carbon atoms such as benzyl group or phenethyl group is preferred.

The "C_{1-22} alkoxy group" used in the specification of the present application means a group corresponding to the

above-defined "C_{1-22} alkyl group" to which end an oxygen atom is bonded. Suitable examples thereof are methoxy group, ethoxy group, n-propoxy group, iso-propoxy group, n-butoxy group, iso-butoxy group, sec-butoxy group, tert-butoxy group, n-pentyloxy group, iso-pentyloxy group, sec-pentyloxy group, n-hexyloxy group, iso-hexyloxy group, 1,1-dimethylpropoxy group, 1,2-dimethylpropoxy group, 2,2-dimethylpropoxy group, 2-ethylpropoxy group, 1-ethyl-2-methylpropoxy group, 1,1,2-trimethylpropoxy group, 1,2,2-trimethylpropoxy group, 1,1-dimethylbutoxy group, 1,2-dimethylbutoxy group, 2,2-dimethylbutoxy group, 2,3-dimethylbutoxy group, 1,3-dimethylbutoxy group, 2-ethylbutoxy group, 1,3-dimethylbutoxy group, 2-methylpentyloxy group, 3-methylpentyloxy group and hexyloxy group.

The "unsaturated C_{2-22} alkoxy group" used in the specification of the present application means a group corresponding to the above-defined "unsaturated C_{2-22} alkyl group" to which end an oxygen atom is bonded. Suitable examples thereof are vinyloxy group, allyloxy group, 1-propenyloxy group, isopropenyloxy group, 2-methyl-1-propenyloxy group, 2-methyl-2-propenyloxy group, 1-butenyloxy group, 2-butenyloxy group, 3-butenyloxy group, 1-pentenyloxy group, 1-hexenyloxy group, 1,3-hexadienyloxy group, 1,5-hexadienyloxy group, propargyloxy group and 2-butynyloxy group.

The "C_{6-14} aryloxy group" used in the specification of the present application means a group corresponding to the

above-defined "C_{6-14} aryl group" to which end an oxygen atom is bonded. Specific examples thereof are phenoxy group, indenyloxy group, 1-naphthyloxy group, 2-naphthyloxy group, azulenyloxy group, heptalenyloxy group, indacenyloxy group, acenaphthyloxy group, fluorenyloxy group, phenalenyloxy group, phenanthrenyloxy group and anthracenyloxy group.

The "5-membered to 14-membered heteroaryloxy group" used in the specification of the present application means a group corresponding to the above-defined "5-membered to 14-membered heteroaryl group" to which end an oxygen atom is bonded. Specific examples thereof are pyrrolyloxy group, pyridinyloxy group, pyridazinyloxy group, pyrimidinyloxy group, pyrazinyloxy group, triazolyloxy group, tetrazolyloxy group, benzotriazolyloxy group, pyrazolyloxy group, imidazolyloxy group, benzimidazolyloxy group, indolyloxy group, isoindolyloxy group, indolizinyloxy group, purinyloxy group, indazolyloxy group, quinolinyloxy group, isoquinolinyloxy group, quinolizinyloxy group, phthalazinyloxy group, naphthyridinyloxy group, quinoxalinyloxy group, quinazolinyloxy group, cinnolinyloxy group, pteridinyloxy group, imidazotriazinyloxy group, pyrazinopyridazinyloxy group, acridinyloxy group, phenanthridinyloxy group, carbazolyloxy group, carbazolinyloxy group, perimidinyloxy group, phenanthrolinyloxy group, phenazinyloxy group, imidazopyridinyloxy group, imidazopyrimidinyloxy group, pyrazolopyridinyloxy group, pyrazolopyridinyloxy group, thienyloxy group, benzothienyloxy

group, furyloxy group, pyranyloxy group, cyclopentapyranyloxy group, benzofuryloxy group, isobenzofuryloxy group, thiazolyloxy group, isothiazolyloxy group, benzothiazolyloxy group, benzothiadiazolyloxy group, phenothiazinyloxy group, isoxazolyloxy group, furazanyloxy group, phenoxazinyloxy group, oxazolyloxy group, isoxazoyloxy group, benzoxazolyloxy group, oxadiazolyloxy group, pyrazolooxazolyloxy group, imidazothiazolyloxy group, thienofuranyloxy group, furopyrrolyloxy group and pyridoxazinyloxy group, of which a preferred example is thienyloxy group, furyloxy group, pyridyloxy group, pyridazyloxy group, pyrimidyloxy group or pyrazyloxy group.

The "5-membered to 14-membered heteroaryloxyalkyl group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-6} alkyl group" which is substituted with the above-defined "5-membered to 14-membered heteroaryloxy group".

The "C_{1-22} alkylsulfonyl group" used in the specification of the present application means a sulfonyl group to which the above-defined "C_{1-22} alkyl group" is bound. Specific examples thereof are methanesulfonyl group, ethanesulfonyl group, n-propanesulfonyl group and iso-propanesulfonyl group.

The "C_{6-14} arylsulfonyl group" used in the specification of the present application means a sulfonyl group to which the above-defined "C_{6-14} aryl group" is bound. Specific examples thereof are benzenesulfonyl group, 1-naphthalenesulfonyl group

and 2-naphthalenesulfonyl group.

The "C_{1-22} alkylsulfonyloxy group" used in the specification of the present application means a group corresponding to the above-defined "C_{1-22} alkylsulfonyl group" to which end an oxygen atom is bonded. Examples thereof are methylsulfonyloxy group, ethylsulfonyloxy group, n-propylsulfonyloxy group and iso-propylsulfonyloxy group.

Examples of the substituent in the term "may have a substituent" used in the specification of the present application include those selected from the group consisting of:

(1) halogen atom;

(2) hydroxyl group;

(3) thiol group;

(4) nitro group;

(5) nitroso group;

(6) cyano group;

(7) carboxyl group;

(8) sulfonyloxy group;

(9) amino group;

(10) a C_{1-22} alkyl group (for example, methyl group, ethyl group, n-propyl group, iso-propyl group, n-butyl group, iso-butyl group, sec-butyl group and tert-butyl group);

(11) an unsaturated C_{2-22} alkyl group (for example, vinyl group, allyl group, 1-propenyl group, isopropenyl group, ethynyl group, 1-propinyl group, 2-propinyl group, 1-butynyl group, 2-butynyl group and 3-butynyl group);

(12) a C_{6-14} aryl group (for example, phenyl group, 1-naphthyl group and 2-naphthyl group);

(13) a 5-membered to 14-membered heteroaryl group (for example, thienyl group, furyl group, pyridinyl group, pyridazinyl group, pyrimidinyl group and pyrazinyl group);

(14) a 3-membered to 14-membered nitrogen-containing non-aromatic heterocyclic group (for example, aziridinyl group, azetidyl group, pyrrolidinyl group, pyrrolyl group, piperidinyl group, piperazinyl group, imidazolyl group, pyrazolidinyl group, imidazolidinyl, morpholinyl group, imidazolinyl group, oxazolinyl group and quinuclidinyl group);

(15) a C_{1-22} alkoxy group (for example, methoxy group, ethoxy group, n-propoxy group, iso-propoxy group, sec-propoxy group, n-butoxy group, iso-butoxy group, sec-butoxy group and tert-butoxy group);

(16) a C_{6-14} aryloxy group (for example, phenoxy group, 1-naphthyloxy group and 2-naphthyloxy group);

(17) a C_{7-22} aralkyloxy group (for example, benzyloxy group, phenethyloxy group, 3-phenylpropyloxy group, 4-phenylbutyloxy group, 1-naphthylmethyloxy group and 2-naphthylmethyloxy group);

(18) a 5-membered to 14-membered heteroaryloxy group (for example, thienyloxy group, furyloxy group, pyridinyloxy group, pyridazinyloxy group, pyrimidinyloxy group and pyrazinyloxy group);

(19) a C_{2-23} alkanoyl group (for example, acetyl group, propionyl

group, butyryl group, iso-butyryl group, valeryl group, iso-valeryl group, pivalyl group, caproyl group, decanoyl group, lauroyl group, myristoyl group, palmitoyl group, stearoyl group and arachidoyl group);

(20) a C_{7-15} aroyl group (for example, benzoyl group, 1-naphthoyl group and 2-naphthoyl group);

(21) a C_{3-23} unsaturated alkanoyl group (for example, acryloyl group, propioloyl group, crotonoyl group, iso-crotonoyl group, oleloyl group and linolenoyl group);

(22) a C_{2-23} alkanoyloxy group (for example, acetoxy group, propionyloxy group and acryloxy group);

(23) a C_{2-22} alkoxycarbonyl group (for example, methoxycarbonyl group, ethoxycarbonyl group, n-propoxycarbonyl group, iso-propoxycarbonyl group, n-butoxycarbonyl group, iso-butoxycarbonyl group, sec-butoxycarbonyl group and tert-butoxycarbonyl group);

(24) an unsaturated C_{3-22} alkoxycarbonyl group (for example, vinyloxycarbonyl group, aryloxycarbonyl group, 1-propenyloxycarbonyl group, isopropenyloxycarbonyl group, propalgyloxycarbonyl group and 2-butynyloxycarbonyl group);

(25) a C_{1-22} alkylsulfonyl group (for example, methanesulfonyl group, ethanesulfonyl group, n-propanesulfonyl group and iso-propanesulfonyl group);

(26) a C_{6-14} arylsulfonyl group (for example, benzenesulfonyl group, 1-naphthalenesulfonyl group and 2-naphthalenesulfonyl group); and

(27) a C_{1-22} alkylsulfonyloxy group (for example, methanesulfonyloxy group, ethanesulfonyloxy group, n-propanesulfonyloxy group and iso-propanesulfonyloxy group).

Examples

Reference Example 1 Production of starting material, a macrolide compound 11107B

One loopful of the slant culture (ISP-2 medium) of Streptomyces sp. Mer-11107 strain (FERM BP-7812) was inoculated into a 500 mL Erlenmeyer flask containing 50 mL of seed medium (2% of glucose, 1% of ESUSAN-MEAT manufactured by Ajinomoto Co. Ltd., 0.5% of yeast extract (manufactured by Oriental Yeast Co., Ltd.), 0.25% of sodium chloride, 0.32% of calcium carbonate, pH 6.8 before sterilization), and it was incubated at 28°C for two days to give the first seed culture broth. 0.1 mL of the culture broth was inoculated into a 500 mL Erlenmeyer flask containing 100 mL of the same seed medium and it was incubated at 28°C for one day to give the second seed culture broth. The second seed culture broth (800 mL) thus obtained was inoculated into a 200 L tank containing 100 L of a production medium (5% of soluble starch, 0.8% of Pharmamedia, 0.8% of gluten meal, 0.5% of yeast extract and 0.1% of calcium carbonate, pH 6.8 before sterilized) and it was cultured for five days with flowing air and stirring under the conditions of a a culture temperature of 28°C, an agitation rotation of 90 rpm, a quantity of aeration of 1.0 vvm and an internal pressure of 20 kPa, to give a culture

broth.

A part of the culture broth (10 L) thus obtained was extracted with 10 L of 1-butanol, and then the resulting butanol layer was evaporated to dryness, to give 100 g of crude active fraction. The crude active fraction was applied on Sephadex LH-20 (1500 mL; manufactured by Pharmacia Co. Ltd.), and eluted with tetrahydrofuran-methanol (1:1) as a solvent. An eluted fraction from 540 mL to 660 mL was concentrated to dryness, to give a residue (660 mg). The resulting residue was dissolved in a mixture of ethyl acetate and methanol (9:1; v/v) and subjected to silica gel column chromatography (WAKO GEL C-200, 50 g). The column was eluted with a mixture (2 L) consisting of n-hexane and ethyl acetate (1:9, v/v), the fractions eluted from 468 mL to 1260 mL were collected, evaporated to give 25 mg of a crude active fraction.

The obtained crude active fraction was subjected to preparative high performance liquid chromatography (HPLC) under the following preparative HPLC condition (A), and the fractions eluted at the retention time of 34 minutes were collected. After removing acetonitrile, the respective fractions were desalted by HPLC under the following preparative HPLC condition (B) to give the maclolide compound 11107B (Retention time: 37 minutes, 6 mg).

Preparative HPLC conditions A:

Column: YMC-PACK ODS-AM SH-343-5AM, φ20 mm × 250 mm (manufactured by YMC Co.)

Temperature: room temperature

Flow rate: 10 mL/min.

Detection: 240 nm

Eluent: acetonitrile/0.15% aqueous potassium dihydrogenphosphate (pH 3.5) (2:8 to 8:2, v/v, 0 to 50 min., linear gradient)

Preparative HPLC conditions B:

Column: YMC-PACK ODS-AM SH-343-5AM, φ20 mm × 250 mm (manufactured by YMC Co.)

Temperature: room temperature

Flow rate: 10 ml/min.

Detection: 240 nm

Eluent: methanol/water (2:8 to 10:0, v/v, 0 to 40 minutes, linear gradient)

Example 1 Determination of the nucleotide sequence of a gene derived from Streptmyces sp. A-1544 strain (FERM BP-8446)

(1) Preparation of a DNA of Streptmyces sp. A-1544 strain chromosome

The A-1544 strain was inoculated into a medium containing 1% of glucose, 0.4% of malt extract and 1% of yeast extract and incubated at 28°C for 3 days. The obtained culture broth was centrifuged at 3000 rpm for 10 minutes to collect the mycelia. A chromosome DNA was prepared using Blood & Cell Culture kit (QIAGEN Co.) from the mycelia.

(2) Cloning of a partial sequence of a DNA encoding a protein having the activity in hydroxylating the 16-position of the

macrolide compound 11107

Mix primers 5Dm-3F (sequence no. 4) and 5Dm-3R (sequence No. 5) were designed and produced on reference to the amino acid sequence assumed to be that of the cytochrome P450 (CYP105D5) of Streptmyces coelicolor A3 (2).

In order to promote reactivity taking the fluctuation of a codon into account, mixed bases S(=C+G) and Y(=C+T) were used.

Next, these two types of primers (5Dm-3F and 5Dm-3R) and the A-1544 strain chromosome DNA obtained in the above (1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a three-stage reaction including denaturing run at 98°C for 20 seconds, annealing run at 50°C for 2 minutes and extension run at 68°C for 30 seconds 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.). As a result, a DNA fragment (hereinafter referred to as a DNA fragment-A1) having a size of about 500 bp was amplified. It is highly possible that this DNA fragment-A1 is a part of the DNA encoding a protein having hydroxylating activity. The DNA fragment-A1 amplified by a PCR reaction was recovered from the reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

In order to obtain the DNA fragment-A1 in an amount enough to analyze the nucleotide sequence of the obtained DNA fragment-A1, the DNA fragment was combined with a plasmid vector pT7Blue T (Novagen Co.) by using DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.) to transform E.coli JM109 strain. Thereafter,

the transformed E. coli was selected using a L-broth agar media (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl, 1.5% agar) containing ampicillin (50 μg/mL), X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside; 40 μg/mL) and IPTG (isopropyl-β-D-thiogalactopyranoside; 100 μM). The colony of the transformed E. coli thus isolated was cultured in a L-broth liquid medium (1% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing ampicillin (50 μg/mL). A plasmid DNA was separated from the mycelia of the proliferated transformed E. coli and purified by using a plasmid purifying kit (QIA filter Plasmid Midi Kit, QIAGEN Co.), to obtain enough amount of the DNA fragment-A1.

(3) Analysis of the nucleotide sequence of the cloned DNA fragment-A1

The nucleotide sequence of the DNA fragment-A1 obtained in the above (2) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. As the result of the nucleotide sequence analysis, it was clarified that the DNA fragment-A1 amplified by a PCR reaction had an exact size of 528 bp though it had been found to have a size of about 500 bp by the above measurement using electrophoresis (see the nucleotide sequence 1775 to nucleotide sequence 2302 of the sequence No. 1). Sinces DNA sequences corresponding to the two types of primers used in the above PCR reaction were found at both ends of the above cloned 528 bp DNA sequence, it was clarified that the DNA fragment-A1

was singularly amplified by these two types of primers (5Dm-3F and 5Dm-3R) in the above PCR reaction.

(4) Analysis of the neighboring region of the DNA fragment-A1

As mentioned above, the partial sequence of the DNA encoding a protein which was derived from the A-1544 strain and had hydroxylating activity. Therefore, the amplification, cloning and sequence analysis of the nucleotide sequence in the neighboring region extending from the upstream side to downstream side of the cloned fragment were accomplished by an inverse PCR method (Cell Technology vol. 14, p.591-593, 1995). Specifically, the A-1544 strain chromosome DNA (see the above (1)) was digested by respective restriction enzymes PstI and SalI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 10 mM dithiothreitol and 100 mM NaCl). The obtained each DNA fragment cut by the restriction enzymes was self-circularized by using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.).

On the other hand, primers (6PIN-2F (sequence No. 6) and 6PIN-2R (sequence No. 7) were designed and produced based on the nucleotide sequence of the DNA fragment-A1.

Next, these two primers (6PIN-2F and 6PIN-2R) and the above self-cyclized A-1544 strain chromosome DNA as a template, were used to run a PCR reaction. In the PCR reaction, the cycle of a two-stage reaction involving denaturing run at 98°C for 20 seconds and annealing and extension run at 68°C for 5 minutes was repeated 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (DNA fragment-B1) about 3.5 kbp in size and a DNA fragment (DNA fragment-C1) about 2.8 kbp in size were amplified. It was highly possible that these DNA fragments were a DNA encoding a protein having hydroxylating activity and a DNA having a DNA sequence including the upstream and downstream regions of the former DNA.

The DNA fragment-B1 and the DNA fragment-C1 were recovered from the PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.). Next, as to the obtained DNA fragment-B1 and DNA fragment-C1, in order to obtain each DNA fragment in an amount enough to analyze the nucleotide sequence of the obtained DNA fragment, a plasmid vector pT7Blue T (Novagen Co.), DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.), E. coli JM109 strain and a plasmid purifying kit (QIA filter Plasmid Midi kit, QIAGEN Co.) were used in the same manner as the above (2), to obtain enough amount of each DNA fragment.

(5) Analysis of each nucleotide sequence of the DNA fragment-B1 (about 3.5 kbp in size) and the DNA fragment-C1 (about 2.8 kbp in size)

Each nucleotide sequence of the DNA fragment-B1 and DNA fragment-C1 obtained in the above (4) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. The nucleotide sequence was thus analyzed to obtain the information of the nucleotide sequence of 3793 bp shown in the sequence No. 1 from each sequence of the DNA fragment-B1 and DNA fragment-C1.

An open reading frame (ORF) in this 3793 bp was retrieved, to find that the two proteins were coded. Each amino acid sequence of these proteins was retrieved by the BLAST search, and as a result, an ORF (hereinafter referred to as psmA) coding a protein consisting of 409 amino acids having high homology to cytochrome P450 existed in the base 1322 to base 2548 of the sequence No. 1. The psmA had the highest homology (homology: 72.6%) to the amino acid sequence assumed to be that of cytochrome P450 (CYP105D5) of the Streptmyces coelicolor A3 (2) and to the amino acid sequence assumed to be that of cytochrome P450 (CYP105D4) of the Streptmyces lividans, and also had a relatively high homology (homology: 69.4%) to cytochrome P450 soy (Soy C) of Streptmyces griseus. It was considered from this fact that the psmA was highly possibly a gene coding hydroxylating enzyme of the cytochrome P-450 type.

Also, an ORF (hereinafter referred to as psmB) encoding a protein having a high homology to ferredoxin of a 3F-4S type existed just downstream (the base 2564 to base 2761 of the sequence No. 1) of the psmA. The protein encoded by the psmB consists of 66 amino acids, and had the highest homology (83.3%) to the amino acid sequence assumed to be that of ferredoxin just downstream of the amino acid sequence assumed to be that of cytochrome P450 (CYP105D5) of the Streptmyces coelicolor A3(2) and a relatively higher homology (homology: 57.6%) to ferredoxin soy (soyB) of Streptmyces griseus. Therefore, it was considered that the psmB serves to transfer electrons and codes ferredoxin

participating in hydroxylation together with the psmA.

Example 2 Production of a transformant having the psmA and the psmB

(1) Preparation of a DNA fragment containing both the psmA and the psmB derived from the A-1544 strain

A primer DM-NdeF (sequence No. 8) obtained by adding a NdeI site to the 5' terminal and a primer DM-SpeR (sequence No. 9) obtained by adding a SpeI site to the 5' terminal were designed and produced on reference to the nucleotide sequence of the sequence No. 1 analyzed in Example 1. Next, these two types of primers (DM-NdeF and DM-SpeR) and the A-1544 strain chromosome DNA obtained in Example 1(1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a two-stage reaction including denaturing carried out at 98°C for 20 seconds and annealing and elongation carried out at 68°C for 2 minutes 30 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (hereinafter referred to as a DNA fragment-D1) having a size of about 1.5 kbp and containing the psmA and the psmB was amplified. The DNA fragment-D1 was recovered from this PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

(2) Architecture of a plasmid pTC-DM

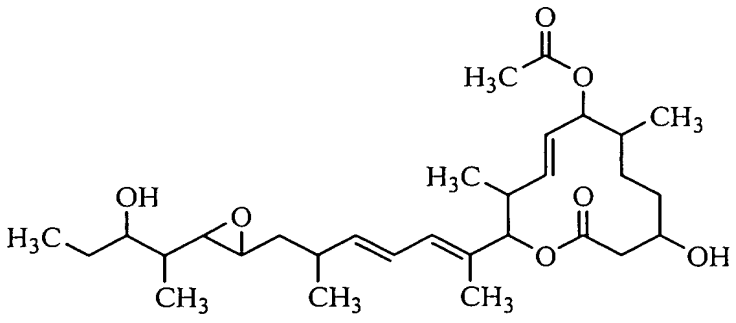
pT7NS-CamAB (see WO03/087381) was digested by respective restriction enzymes NdeI and SpeI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 10 mM dithiothreitol and 100

mM NaCl) to obtain a plasmid digested products. Similarly, the DNA fragment-D1 obtained in the above (1) was digested by respective restriction enzymes NdeI and SpeI. The obtained digested product of the DNA fragment-D1 and the plasmid digested product were coupled using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.). This resulted in the formation of a plasmid (referred to as a plasmid pTC-DM) about 9.5 kbp in size which was an architecture of a combination of the DNA fragment-D1 containing both the psmA and the psmB therein and the plasmid pT7NS-CamAB.

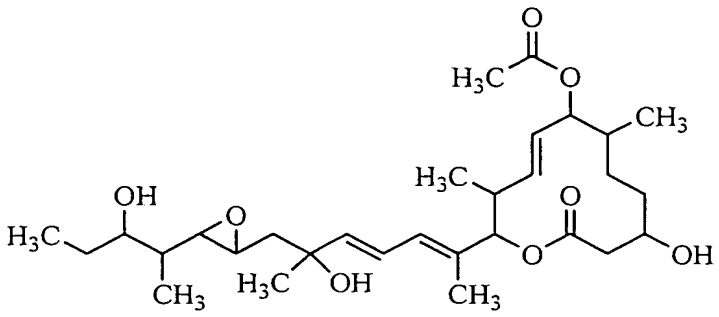
(3) Preparation of E. coli transforming strain BL21 (DE3)/pTC-DM

Using the plasmid pTC-DM prepared in the above (2), a competent cell (Novagen) of Colibacillus BL21 (DE3) was transformed. E. coli BL21 (DE3)/pTC-DM strain transformed by the plasmid pTC-DM was obtained.

Example 3: Conversion of ME-265 into ME-282 represented by the following formulae by the E. coli transformant having the psmA and the psmB



ME-265



ME-282

(1) Preparation of a transformant reaction solution

The transformed E. coli BL21(DE3)/pTC-DM strain obtained in Example 2(3) and a frozen seed of a BL21(DE3)/pT7NS-CamAB strain were inoculated into a 15 mL test tube containing 3 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 37°C for 20 hours. 500 μL of the seed culture broth was inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 32°C for 3 hours. Then, 50 μL of 100 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and 50 μL of 80 mg/mL 5-aminolevulinic acid were successively added thereto, and the medium was shake-cultured at 32°C for 6 hours. The obtained culture broth was centrifuged (5000 rpm, 10 minutes) to collect the mycelia. The mycelia were then suspended in 1.75 mL of a 100 mM phosphate buffer solution (pH 6.1), and 250 μL of 80% glycerol and 50 μL of 8 mg/mL ME-265 were added thereto. The conversion reaction solution thus obtained was reacted at 28°C for 24 hours. 200 μL of the reaction solution was extracted

with 1 mL of acetonitrile and the extract was subjected to HPLC to measure each amount of ME-265 and ME-282. The results are shown in Table 3.

Also, the details of the condition of HPLC are shown below.

Analyzer: Shimadzu HPLC 10Avp

Column: CAPCELL PAK C18 SG120 (φ4.6 mm × 250 mm)

Mobile phase: 45% acetonitrile (0 to 15 minutes)

60% acetonitrile (15 to 30 minutes)

45% acetonitrile (30 to 45 minutes)

Flow rate: 1 mL/min.

Detection: UV 240 nm

Injection capacity: 10 μL

Column temperature: 40°C

Analyzing time: 45 minutes

Retention time: ME-265 24.8 minutes

ME-282 12.7 minutes

Table 3

mg/L	BL21(DE3)/pT7NS-CamAB	BL21(DE3)/pTC-DM
ME-265	143	0
ME-282	0	130

(2) Isolation of ME-282 from the transformant reaction solution

4 mL of water was added to 1.8 mL of the reaction solution that had been reacted for 24 hours and the reaction solution was then extracted with 8 mL of ethyl acetate once and with 4 mL of ethyl acetate twice. The ethyl acetate layers were combined, dried over anhydrous sodium sulfate and then the solvent was

removed. The resulting residue was purified by thin layer chromatography (MERCK Silicagel 60 F254 0.25 mm, developing solution: hexane:ethyl acetate=1:2), to give 0.2 mg of ME-282.

^{1}H-NMR spectrum (CD_3OD, 500MHz): δ ppm (integral, multiplicity, coupling constant J(Hz)):
0.87(3H,d,J=7.0Hz), 0.90(3H,d,J=7.0Hz), 0.94(3H,t,J=7.3Hz), 0.97(3H,d,J=6.6Hz), 1.21-1.26(1H,m), 1.29-1.37(3H,m), 1.34(3H,s), 1.44-1.52(2H,m), 1.60-1.64(1H,m), 1.65(1H,dd,J=6.2,13.9Hz), 1.77(3H,d,J=1.1Hz), 1.86(1H,dd,J=5.4,13.9Hz), 1.89-1.94(1H,m), 2.00(3H,s), 2.43(1H,dd,J=5.5,13.9Hz), 2.50-2.60(1H,m), 2.56(1H,dd,J=3.3,13.9Hz), 2.66(1H,dd,J=2.2,7.7Hz), 2.89(1H,dt,J=2.2,6.2Hz), 3.52(1H,dt,J=4.8,8.4Hz), 3.75-3.80(1H,m), 4.90(1H,overlapped with D_2O), 5.01(1H,d,J=10.6Hz), 5.42(1H,dd,J=9.2,15.0Hz), 6.13(1H,d,J=10.6Hz), 6.52(1H,dd,J=11.0,15.0Hz).

As a result, a peak estimated as that of ME-282 was not observed in the case of the E. coli BL21(DE3)/pT7NS-CamAB strain used as a control, whereas ME-265 was almost consumed and a peak estimated as that of ME-282 was obtained in the case of the BL21(DE3)/pTC-DM strain containing the psmA and psmB. This fact suggests that the psmA and the psmB participate in the conversion of ME-265 into ME-282.

Example 4: Conversion of the macrolide compound 11107B into the macrolide compound 11107D by the E. coli transformant having the psmA and the psmB

(1) Preparation of a transformant reaction solution

A test using the macrolide compound 11107B as a substrate was made in the same manner as Example 3. The transformed E. coli BL21(DE3)/pTC-DM strain obtained in Example 2(3) and a frozen seed of a BL21(DE3)/pT7NS-CamAB strain were inoculated into a 15 mL test tube containing 3 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 30°C for 20 hours. 500 μL of the seed culture broth was inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 28°C for 5 hours. Then, 50 μL of 100 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and 50 μL of 80 mg/mL 5-aminolevulinic acid were successively added and the medium was shake-cultured at 25°C for 20 hours. The obtained culture broth was centrifuged (5000 rpm, 10 minutes) to collect the mycelia. The mycelia were then suspended in 1.75 mL of a 100 mM phosphate buffer solution (pH 6.1), and 250 μL of 80% glycerol and 50 μL of 40 mg/mL 11107B were added thereto. The conversion reaction solution thus obtained was reacted at 28°C for 24 hours. 200 μL of the reaction solution was extracted with 1 mL of acetonitrile and the extract was subjected to HPLC to measure each amount of the macrolide compound 11107B and the macrolide compound 11107D. The results are shown in Table 4. Also, the details of the condition of HPLC are shown below.

Analyzer: Shimadzu HPLC 10Avp

Column: CAPCELL PAK C18 SG120 (φ4.6 mm × 250 mm)

Mobile phase: 35% acetonitrile (0 to 10 minutes)

35% to 65% acetonitrile (10 to 12 minutes)

65% acetonitrile (12 to 15 minutes)

35% acetonitrile (15 to 20 minutes)

Flow rate: 1 mL/min.

Detection: UV 240 nm

Injection capacity: 10 μL

Column temperature: 40°C

Analyzing time: 20 minutes

Retention time: 11107B 14.3 minutes

11107D 7.9 minutes

Table 4

mg/L	BL21(DE3)/pT7NS-CamAB	BL21(DE3)/pTC-DM
11107B	636	619
11107D	0	71

(2) Isolation of the macrolide compound 11107D from the transformant reaction solution

4 mL of water was added to 1.8 mL of the reaction solution that had been reacted for 24 hours and the mixture was then extracted with 8 mL of ethyl acetate once and with 4 mL of ethyl acetate twice. The ethyl acetate layers were combined, dried over anhydrous sodium sulfate and the solvent was removed. The resulting residue was purified by thin layer chromatography (MERCK Silicagel 60 F254 0.25 mm, developing solution: ethyl acetate) to obtain 0.1 mg of 11107D.

^{1}H-NMR spectrum (CD_3OD, 500MHz): δ ppm (integral, multiplicity, coupling constant J(Hz)):

0.87(3H,d,J=7.0Hz), 0.88(3H,d,J=7.0Hz), 0.93(3H,t,J=7.0Hz), 1.18(3H,s), 1.18-1.69(8H,m), 1.33(3H,s), 1.77(3H,d,J=1.1Hz), 1.82-1.90(1H,m), 2.05(3H,s), 2.49-2.60(3H,m), 2.66(1H,dd,J=2.2,8.2Hz), 2.89(1H,dt,J=2.4,5.7Hz), 3.52(1H,dt,J=4.8,8.3Hz), 3.73-3.82(1H,m), 5.04(1H,d,J=9.8Hz), 5.05(1H,d,J=10.6Hz), 5.56(1H,dd,J=9.8,15.2Hz), 5.70(1H,dd,J=9.8,15.2Hz), 5.86(1H,d,J=15.2Hz), 6.3(1H,d,J=10.8Hz), 6.52(1H,dd,J=10.8,15.2Hz).

As a result, a peak estimated as that of the macrolide compound 11107D was not observed in the case of the E. coli BL21(DE3)/pT7NS-CamAB strain used as a control, whereas a peak estimated as that of the macrolide compound 11107D was obtained in the case of the BL21(DE3)/pTC-DM strain containing the psmA and psmB. This fact suggests that the psmA and the psmB participate in the conversion of macrolide compound 11107B into the macrolide compound 11107D.

Example 5: Conversion test using an A-1544 self-cloning strain

(1) Preparation of a DNA fragment containing both the psmA and the psmB derived from the A-1544 strain

A primer DM-BglF (sequence No. 10) obtained by adding a BglII site to the 5′ terminal and a primer DM-BglR (sequence No. 11) obtained by adding a BglII site to the 5′ terminal were designed and produced on reference to the nucleotide sequence of the sequence No. 1 analyzed in Example 1.

Next, these two types of primers (DM-BglF and DM-BglR) and the A-1544 strain chromosome DNA obtained in Example 1(1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a three-stage reaction including denaturing carried out at 98°C for 20 seconds, annealing carried out at 63°C for 30 seconds and elongation carried out at 68°C for 4 minutes 30 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (hereinafter referred to as a DNA fragment-E1) having a size of about 3.5 kbp and containing the psmA and the psmB was amplified. This PCR amplified reaction solution was subjected to agarose gel electrophoresis to fractionate. The above DNA fragment-E1 about 3.5 kbp in size was cut out of the agarose gel and recovered by SUPREC 01 (TAKARA HOLDINGS INC.).

(2) Architecture of a plasmid pIJDMG

pIJ702 was digested by a restriction enzyme BglII in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 10 mM dithiothreitol and 100 mM NaCl) to obtain a plasmid digested products. Similarly, the DNA fragment-E1 obtained in the above (1) was digested by a restriction enzyme BglII. The obtained digested product of the DNA fragment-E1 and the plasmid-digested product were bound using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.). The resulted in the formation of a plasmid (referred to as a plasmid pIJDMG) about 8.5 kbp in size which was an architecture of a combination of the DNA fragment-E1 containing

both the psmA and the psmB therein and the plasmid pIJ702.

(3) Preparation of a self-cloning strain A-1544/pIJDMG strain

Using the plasmid pIJDMG prepared in the above (2), an A-1544 strain was transformed according to the method described in Genetic Manipulation of Streptmyces: A Laboratory Manual. John Innes Foundation, Norwich, 1985. An A-1544/pIJDMG strain was thus obtained by transformation using the plasmid pIJDMG.

Example 6: Conversion of 11107B into 11107D by a self-cloning strain

The transformed A-1544/pIJDMG strain obtained in Example 5(3), A-1544/pIJ702 strain and a frozen seed of the original A-1544 strain were inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a SMN medium (Stabilose 2%, glucose 2%, ESUSAN-MEAT 2%, yeast extract 0.5%, NaCl 0.25%, $CaCO_3$ 0.32%, pH 7.4) containing 25 μg/mL of thiostrepton, and shake-cultured at 28°C for 48 hours (seed culture, no addition of thiostrepton to the A-1544 strain). 0.5 mL of the obtained seed culture broth was inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a SMN medium containing 25 μg/mL of thiostrepton and shake-cultured at 28°C for 72 hours (no addition of thiostrepton to the A-1544 strain). The obtained culture broth was dispensed in 2 mL portions, and 100 μL of a 1M phosphate buffer solution (pH 6.5) and 50 μL of 40 mg/mL of 11107B were added thereto. The conversion culture broth thus obtained was reacted at 28°C for 12 hours. 200 μL of the reaction solution was extracted with 1 mL of acetonitrile and the extract was subjected to HPLC

to measure each amount of 11107B and 11107D. The results are shown in Table 5. Also, the details of the condition of HPLC are shown below.

Analyzer: Shimadzu HPLC 10Avp

Column: CAPCELL PAK C18 SG120 (φ4.6 mm × 250 mm)

Mobile phase: 35% acetonitrile (0 to 10 minutes)
35% to 65% acetonitrile (10 to 12 minutes)
65% acetonitrile (12 to 15 minutes)
35% acetonitrile (15 to 20 minutes)

Flow rate: 1 mL/min.

Detection: UV 240 nm

Injection capacity: 10 μL

Column temperature: 40°C

Analyzing time: 20 minutes

Retention time: 11107B 14.3 minutes
11107D 7.9 minutes

Table 5

mg/L	A-1544 strain	A-1544/pIJ702 strain	A-1544/pIJDMG strain
11107B	496	651	14
11107D	196	0	535

As a result, the A-1544/pIJDMG strain obtained by transformation of the plasmid containing the psmA and the psmB exhibited conversion activity about 2.7 times that of the original A-1544 strain by a reaction run for 12 hours. This fact suggests that the self-cloning of the psmA and psmB contributes to the conversion of the macrolide compound 11107B

into the macrolide compound 11107D.

Example 7 Determination of the nucleotide sequence of a gene derived from Streptmyces sp. Mer-11107 strain (FERM BP-7812)

(1) Preparation of a DNA of Streptmyces sp. Mer-11107 strain chromosome

The Mer-11107 strain was inoculated into a medium containing 1% of glucose, 0.4% of malt extract and 1% of yeast extract and cultured at 28°C for 3 days. The obtained culture broth was centrifuged at 3000 rpm for 10 minutes to collect the mycelia. A chromosome DNA was prepared using Blood & Cell Culture kit (QIAGEN Co.) from the mycelia.

(2) Cloning of a partial sequence of a DNA encoding a protein having the activity in hydroxylating the 16-position of the macrolide compound 11107

Mix primers 5Dm-3F (sequence no. 4) and 5D-1R (sequence No. 12) were designed and produced on reference to the amino acid sequence estimated as that of the cytochrome P450 (CYP105D5) of Streptmyces coelicolor A3(2).

In order to promote reactivity taking the fluctuation of a codon into account, mixed bases S(=C+G) and Y(=C+T) were used.

Next, these two types of primers (5Dm-3F and 5D-1R) and the Mer-11107 strain chromosome DNA obtained in the above (1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a three-stage reaction including denaturing carried out at 98°C for 20 seconds, annealing carried out at 50°C for 2 minutes and elongation carried out at 68°C

for 30 seconds 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.). As a result, a DNA fragment (hereinafter referred to as a DNA fragment-A2) having a size of about 300 bp was amplified. It is highly possible that the DNA fragment-A2 is a part of the DNA encoding a protein having hydroxylating activity. The DNA fragment-A2 amplified by a PCR reaction was recovered from the reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

In order to obtain the DNA fragment-A2 in an amount enough to analyze the nucleotide sequence of the obtained DNA fragment-A2, the DNA fragment was bound with a plasmid vector pT7Blue T (Novagen Co.) by using DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.) to transform E. coli JM109 strain. Thereafter, the transformed E. coli was selected using a L-broth agar media (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl, 1.5% agar) containing ampicillin (50 μg/mL), X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside; 40 μg/mL) and IPTG (isopropyl-β-D-thiogalactopyranoside; 100 μM). The colony of the transformed E. coli thus isolated was cultured in a L-broth liquid medium (1% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing ampicillin (50 μg/mL). A plasmid DNA was separated from the mycelia of the proliferated transformed E. coli and purified by using a plasmid purifying kit (QIA filter Plasmid Midi Kit, QIAGEN Co.), to obtain enough amount of the DNA fragment-A2.

(3) Analysis of the nucleotide sequence of the cloned DNA

fragment-A2

The nucleotide sequence of the DNA fragment-A2 obtained in the above (2) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. As the result of the nucleotide sequence analysis, it was clarified that the DNA fragment-A2 amplified by a PCR reaction had an exact size of 325 bp though it had been found to have a size of about 300 bp by the above measurement using electrophoresis (see the nucleotide sequence 837 to nucleotide sequence 1161 of the sequence No. 2). Since DNA sequences corresponding to the two types of primers used in the above PCR reaction were found at both ends of the above cloned 325 bp DNA sequence, it was clarified that the DNA fragment-A2 was specifically amplified by these two types of primers (5Dm-3F and 5D-1R) in the above PCR reaction.

(4) Analysis of the neighboring region of the DNA fragment-A2

As mentioned above, the partial sequence of the DNA encoding a protein having the hydroxylating activity derived from the Mer-11107 strain was determined. Therefore, the amplification, cloning and sequence analysis of the nucleotide sequence in the neighboring region extending from the upstream side to downstream side of the cloned fragment were accomplished by an inverse PCR method (Cell Technology vol. 14, p.591-593, 1995). Specifically, the Mer-11107 strain chromosome DNA (see the above (1)) was digested by a restriction enzyme BamHI in a K buffer solution (50 mM Tris-HCl, pH 8.5, 10 mM $MgCl_2$, 1 mM dithiothreitol

and 100 mM KCl) and by a restriction enzyme SalI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 1 mM dithiothreitol and 100 mM NaCl) respectively. The obtained each DNA fragment cut by the restriction enzymes was self-circularized using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.).

On the other hand, primers (7PIN-2F (sequence No. 13) and 6PIN-2R (sequence No. 7) were designed and produced based on the nucleotide sequence of the DNA fragment-A2.

Next, these two primers (7PIN-2F and 6PIN-2R) and the above self-circularized Mer-11107 strain chromosome DNA as a template, were used to run a PCR reaction. In the PCR reaction, the cycle of a two-stage reaction involving denaturing carried out at 98°C for 20 seconds and annealing and elongation carried out at 68°C for 5 minutes was repeated 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (DNA fragment-B2) about 1.3 kbp in size and a DNA fragment (DNA fragment-C2) about 1.4 kbp in size were amplified. It was highly possible that these DNA fragments were respectively a DNA encoding a protein having hydroxylating activity and a DNA having a DNA sequence including those in the upstream and downstream regions of the former DNA.

The DNA fragment-B2 and the DNA fragment-C2 were recovered from the PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.). Next, as to the obtained DNA fragment-B2 and DNA fragment-C2, in order to obtain each DNA fragment in an amount enough to analyze the nucleotide sequence of the obtained DNA

fragment, a plasmid vector pT7Blue T (Novagen Co.), DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.), E. coli JM109 strain and a plasmid purifying kit (QIA filter Plasmid Midi Kit, QIAGEN Co.) were used in the same manner as the above (2), to obtain enough amount of each DNA fragment.

(5) Analysis of each nucleotide sequence of the DNA fragment-B2 (about 1.3 kbp in size) and the DNA fragment-C2 (about 1.4 kbp in size)

Each nucleotide sequence of the DNA fragment-B2 and DNA fragment-C2 obtained in the above (4) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. The nucleotide sequence was thus analyzed to obtain the information of the nucleotide sequence of 2329 bp shown in the sequence No. 2 from each sequence of the DNA fragment-B2 and DNA fragment-C2.

An open reading frame (ORF) in this 2329 bp was retrieved, to find that the two kinds of protein were coded. Each amino acid sequence of these proteins was retrieved by the BLAST search, and as a result, an ORF (hereinafter referred to as bpmA) encoding a protein consisting of 395 amino acids having high homology to cytochrome P450 existed in the base 420 to base 1604 of the sequence No. 2. The bpmA had the highest homology (homology: 67.4%) to the amino acid sequence of the psmA isolated from the A-1544 strain and also had a relatively high homology (homology: 64.8%) to cytochrome P450 soy (Soy C) of Streptmyces griseus. It was considered from this fact that the bpmA highly possibly

encoded hydroxyllating enzyme of the cytochrome P-450 type.

Also, an ORF (hereinafter referred to as bpmB) encoding a protein having a high homology to ferredoxin of a 3Fe-4S type that existed just downstream (the base 1643 to base 1834 of the sequence No. 2) of the bpmA. The protein encoded by the bpmB consisted of 64 amino acids, and had the highest homology (81.0%) to the amino acid sequence of the psmB isolated from the A-1544 strain and a relatively higher homology (homology: 76.2%) to the amino acid sequence assumed to be that of ferredoxin just downstream of the amino acid sequence assumed to be cytochrome P450 (CYP105D5) of Streptmyces coelicolor A3(2). Therefore, it was considered that the bpmB served to transfer electrons and participated in hydroxylation together with the bpmA.

Example 8 Production of a transformant having the bpmA and the bpmB

(1) Preparation of a DNA fragment containing both the bpmA and the bpmB derived from the Mer-11107 strain

A primer 07-NdeF (sequence No. 14) obtained by adding a NdeI site to the 5' terminal and a primer 07-SpeR (sequence No. 15) obtained by adding a SPeI site to the 5' terminal were designed and produced on reference to the nucleotide sequence of the sequence No. 2 analyzed in Example 7. Next, these two types of primers (07-NdeF and 07-SpeR) and the Mer-11107 strain chromosome DNA obtained in Example 7(1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a two-stage reaction including denaturing carried out

at 98°C for 20 seconds and annealing and elongation carried out at 68°C for 2 minutes 30 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (hereinafter referred to as a DNA fragment-D2) having a size of about 1.5 kbp and containing the psmA and the psmB was amplified. The DNA fragment-D2 was recovered from the PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

(2) Architecture of a plasmid pTC-D07

pT7NS-CamAB (see WO03/087381) was digested by respective restriction enzymes NdeI and SpeI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 1 mM dithiothreitol and 100 mM NaCl) to obtain a plasmid digested products. Similarly, the DNA fragment-D2 obtained in the above (1) was digested by respective restriction enzymes NdeI and SpeI. The obtained digested product of the DNA fragment-D2 and the plasmid digested product were bound using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.). Thereby, a plasmid (referred to as a plasmid pTC-D07) about 9.5 kbp in size which was an architecture of a combination of the DNA fragment-D2 containing both the bpmA and the bpmB therein and the plasmid pT7NS-CamAB was formed.

(3) Preparation of E. coli transforming strain BL21 (DE3)/pTC-D07

Using the plasmid pTC-D07 prepared in the above (2), a competent cell (Novagen) of Colibacillus BL21 (DE3) was transformed. Thereby, E. coli BL21 (DE3)/pTC-D07 strain transformed by the plasmid pTC-D07 was obtained.

Example 9: Conversion of the macrolide compound 11107B into the 11107D by the E. coli transformant having the bpmA and the bpmB

The transformed E. coli BL21(DE3)/pTC-D07 strain obtained in Example 8(3) and a frozen seed of a BL21(DE3)/pT7NS-CamAB strain were inoculated into a 15 mL test tube containing 3 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 37°C for 20 hours. 500 μL of the seed culture broth was inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 32°C for 4 hours. Then, 50 μL of 100 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and 50 μL of 80 mg/mL 5-aminolevulinic acid were successively added and the medium was shake-cultured at 32°C for 5 hours. The obtained culture broth was centrifuged (5000 rpm, 10 minutes) to collect the mycelia. The mycelia were then suspended in 1.75 mL of a 100 mM phosphate buffer solution (pH 6.1), to which were then added 250 μL of 80% glycerol and 12.5 μL of 40 mg/mL macrolide compound 11107B. The conversion reaction solution obtained in this manner was reacted at 28°C for 24 hours. 400 μL of the reaction solution was extracted with 600 μL of methanol and the extract was subjected to HPLC to measure each amount of macrolide compounds 11107B and 11107D. The results are shown in Table 6.

Also, the details of the condition of HPLC are shown below.

Analyzer: Shimadzu HPLC 10Avp

Column: Develosil ODS UG-3 (φ4.6 mm × 250 mm 3 μm)

Mobile phase: 45% to 55% methanol (0 to 5 minutes)

55% methanol (5 to 13 minutes)

55% to 70% methanol (13 to 17 minutes)

70% methanol (17 to 21 minutes)

45% methanol (21 to 25 minutes)

Flow rate: 1.2 mL/min.

Detection: UV 240 nm

Injection capacity: 5 μL

Column temperature: 40°C

Analyzing time: 25 minutes

Retention time: 11107B 12.2 minutes

11107D 4.2 minutes

Table 6

mg/L	BL21(DE3)/pT7NS-CamAB	BL21(DE3)/pTC-D07
11107B	162	156
11107D	0.00	0.78

As a result, the peak of the macrolide compound 11107D was not observed in the case of the E. coli BL21(DE3)/pT7NS-CamAB strain used as a control, whereas the peak of the macrolide compound 11107D was obtained in the case of the BL21(DE3)/pTC-D07 strain containing the psmA and psmB. This fact suggests that the bpmA and the bpmB participate in the conversion of the macrolide compound 11107B into the macrolide compound 11107D.

Example 10 Determination of the nucleotide sequence of a gene

derived from the A-1560 strain (FERM BP-10102)

(1) Preparation of a DNA of the A-1560 strain chromosome

The A-1560 strain was inoculated into a medium containing 1% of glucose, 0.4% of malt extract and 1% of yeast extract and cultured at 28°C for 3 days. The obtained culture broth was centrifuged at 3000 rpm for 10 minutes to collect the mycelia. A chromosome DNA was prepared using Blood & Cell Culture kit (QIAGEN Co.) from the mycelia.

(2) Cloning of a partial sequence of a DNA encoding a protein having the activity in hydroxylating the 16-position of the macrolide compound 11107

Mix primers (5Dm-3F (sequence no. 4) and 5Dm-2R (sequence No. 16) were designed and produced on reference to the amino acid sequence estimated as that of the cytochrome P450 (CYP105D5) of Streptmyces coelicolor A3(2).

In order to promote reactivity taking the fluctuation of a codon into account, mixed bases S (=C+G) and Y (=C+T) were used.

Next, these two types of primers (5Dm-3F and 5Dm-2R) and the A-1560 strain chromosome DNA obtained in the above (1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a three-stage reaction including denaturing carried out at 98°C for 20 seconds, annealing carried out at 50°C for 2 minutes and elongation carried out at 68°C for 30 seconds 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.). As a result,

a DNA fragment (hereinafter referred to as a DNA fragment-A3) having a size of about 750 bp was amplified. It is highly possible that this DNA fragment-A3 is a part of the DNA encoding a protein having hydroxylating activity. The DNA fragment-A3 amplified by a PCR reaction was recovered from the reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

In order to obtain the DNA fragment-A3 in an amount enough to analyze the nucleotide sequence of the obtained DNA fragment-A3, the DNA fragment-A3 was bound with a plasmid vector pT7Blue T (Novagen Co.) by using DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.) to transform E. coli JM109 strain (Stratagene Co.). Thereafter, the transformed E. coli was selected using a L-broth agar media (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl, 1.5% agar) containing ampicillin (50 μg/mL), X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside; 40 μg/mL) and IPTG (isopropyl-β-D-thiogalactopyranoside; 100 μM). The colony of the transformed E. coli thus isolated was cultured in a L-broth liquid medium (1% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing ampicillin (50 μg/mL). A plasmid DNA was separated from the mycelia of the proliferated transformed E. coli and purified by using a plasmid purifying kit (QIA filter Plasmid Midi Kit, QIAGEN Co.), to obtain enough amount of the DNA fragment-A3.

(3) Analysis of the nucleotide sequence of the cloned DNA fragment-A3

The nucleotide sequence of the DNA fragment-A3 obtained

in the above (2) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. As the result of the nucleotide sequence analysis, it was clarified that the DNA fragment-A3 amplified by a PCR reaction had an exact size of 741 bp though it had been found to have a size of about 750 bp by the above measurement using electrophoresis (see the nucleotide sequence 616 to nucleotide sequence 1356 of the sequence No. 3). Since DNA sequences corresponding to the two types of primers used in the above PCR reaction were found at both ends of the above cloned 741 bp DNA sequence, it was clarified that the DNA fragment-A3 was singularly amplified by these two types of primers (5Dm-3F and 5Dm-2R) in the above PCR reaction.

(4) Analysis of the neighboring region of the DNA fragment-A3

As mentioned above, the partial sequence of the DNA encoding a protein having hydroxylating activity derived from the A-1560 strain was determined. Therefore, the amplification, cloning and sequence analysis of the nucleotide sequence in the neighboring region extending from the upstream side to downstream side of the cloned fragment were accomplished by an inverse PCR method (Cell Technology vol. 14, p.591-593, 1995). Specifically, the A-1560 strain chromosome DNA (see the above (1)) was digested by a restriction enzyme BamHI in a K buffer solution (50 mM Tris-HCl, pH 8.5, 10 mM $MgCl_2$, 1 mM dithiothreitol and 100 mM KCl), by a restriction enzyme KpnI in a L buffer solution (10 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$ and 1 mM dithiothreitol)

and by a restriction enzyme SalI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 1 mM dithiothreitol and 100 mM NaCl) respectively. The obtained each DNA fragment cut by the restriction enzymes was self-circularized using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.).

On the other hand, primers (5PIN-2F (sequence No. 17) and 6PIN-2R (sequence No. 7)) were designed and produced based on the nucleotide sequence of the DNA fragment-A3.

Next, these two primers (5PIN-2F and 6PIN-2R) and the above self-circularized A-1560 strain chromosome DNA as a template, were used to run a PCR reaction. In the PCR reaction, the cycle of a two-stage reaction involving denaturing carried out at 98°C for 20 seconds and annealing and elongation carried out at 68°C for 5 minutes was repeated 35 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (DNA fragment-B3) about 4.5 kbp in size, a DNA fragment (DNA fragment-C3) about 3.0 kbp in size and a DNA fragment (DNA fragment-D3) about 1.7 kbp in size were amplified. It was highly possible that these DNA fragments were a DNA encoding a protein having hydroxylating activity and a DNA having a DNA sequence including those in the upstream and downstream regions of the former DNA.

The DNA fragment-B3, the DNA fragment-C3 and the DNA fragment-D3 were recovered from the PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.). Next, as to the obtained DNA fragment-B3, DNA fragment-C3 and DNA fragment-D3,

in order to obtain each DNA fragment in an amount enough to analyze the nucleotide sequence of the obtained DNA fragment, a plasmid vector pT7Blue T (Novagen Co.), DNA Ligation kit ver.2 (TAKARA HOLDINGS INC.), E. coli JM109 strain and a plasmid purifying kit (QIA filter Plasmid Midi Kit, QIAGEN Co.) were used in the same manner as the above (2), to obtain enough amount of each DNA fragment.

(5) Analysis of each nucleotide sequence of the DNA fragment-B3 (about 4.5 kbp in size), the DNA fragment-C3 (about 3.0 kbp in size) and the DNA fragment-D3 (about 1.7 kbp in size)

Each nucleotide sequence of the DNA fragment-B3, DNA fragment-C3 and DNA fragment-D3 obtained in the above (4) was analyzed using a DNA nucleotide sequence analyzer (PE Biosystems 377XL) according to a dye terminator cycle sequence method. The nucleotide sequence was thus analyzed to obtain the information of the nucleotide sequence of 1860 bp shown in the sequence No. 3 from each sequence of the DNA fragment-B3, DNA fragment-C3 and DNA fragment-D3.

An open reading frame (ORF) in this 1860 bp was retrieved, to find that the two kinds of protein were encoded. Each amino acid sequence of these proteins was retrieved by the BLAST search, and as a result, an ORF (hereinafter referred to as tpmA) encoding a protein consisting of 404 amino acids having high homology to cytochrome P450 existed in the base 172 to base 1383 of the sequence No. 3. The tpmA had the highest homology (homology: 77.4%) to the amino acid sequence assumed to be that of cytochrome

P450 (CYP105D5) of Streptmyces coelicolor A3(2) and also a high homology (homology: 76.6%) to the amino acid sequence of the psmA isolated from the A-1544 strain. It was considered from this fact that the tpmA was highly possibly a gene encoding hydroxylating enzyme of the cytochrome P-450 type.

Also, an ORF (hereinafter referred to as tpmB) encoding a protein having a high homology to ferredoxin of a 3Fe-4S type existed just downstream (the base 1399 to base 1593 of the sequence No. 3) of the tpmA. The protein encoded by the tpmB consisted of 65 amino acids, and had the highest homology (81.0%) to the amino acid sequence of the psmB isolated from the A-1544 strain and also a high homology (homology: 82.5%) to the amino acid sequence assumed to be that of ferredoxin just downstream of the amino acid sequence assumed to be cytochrome P450 (CYP105D5) of Streptmyces coelicolor A3 (2). Therefore, it was considered that the tpmB served to transfer electrons and coded ferredoxin participating in hydroxylation together with the tpmA.

Example 11 Production of a transformant having the tpmA and the tpmB

(1) Preparation of a DNA fragment containing both the tpmA and the tpmB derived from the A-1560 strain

A primer tpm-NdeF (sequence No. 18) obtained by adding a NdeI site to the 5' terminal and a primer tpm-SpeR (sequence No. 19) obtained by adding a SPeI site to the 5' terminal were designed and produced on reference to the nucleotide sequence of the sequence No. 3 analyzed in Example 10. Next, these two

types of primers (tpm-NdeF and tpm-SpeR) and the A-1560 strain chromosome DNA obtained in Example 10(1) as a template, were used to run a PCR reaction. The PCR reaction was accomplished by repeating a two-stage reaction including denaturing carried at 98°C for 20 seconds and annealing and elongation carried out at 68°C for 2 minutes 30 times by using Takara LA Taq (TAKARA HOLDINGS INC.) and a PCR amplifier (T Gradient, Biometra Co.).

As a result, a DNA fragment (hereinafter referred to as a DNA fragment-E3) having a size of about 1.5 kbp and containing the tpmA and the tpmB was amplified. The DNA fragment-E3 was recovered from this PCR amplified reaction solution by SUPREC PCR (TAKARA HOLDINGS INC.).

(2) Architecture of a plasmid pTC-tpmAB

pT7NS-CamAB (see WO03/087381) was digested by respective restriction enzymes NdeI and SpeI in a H buffer solution (50 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, 1 mM dithiothreitol and 100 mM NaCl) to obtain plasmid digested products. Similarly, the DNA fragment-E3 obtained in the above (1) was digested by respective restriction enzymes NdeI and SpeI. The obtained digested product of the DNA fragment-E3 and the plasmid digested product were bound using DNA Ligation Kit ver.2 (TAKARA HOLDINGS INC.). Thereby, a plasmid (referred to as a plasmid pTC-tpmAB) about 9.5 kbp in size which was an architecture of a combination of the DNA fragment-E3 containing both the tpmA and the tpmB therein and the plasmid pT7NS-CamAB was formed.

(3) Preparation of E. coli transforming strain BL21

(DE3)/pTC-tpmAB

Using the plasmid pTC-tpmAB prepared in Example 11(2), a competent cell (Novagen) of Colibacillus BL21 (DE3) was transformed, to give E. coli BL21 (DE3)/pTC-tpmAB strain transformed by the plasmid pTC-tpmAB.

Example 12: Conversion of the 11107B into the 11107D by the E. coli transformant having the tpmA and the tpmB

The transformed E. coli BL21(DE3)/pTC-tpmAB strain obtained in the above (3) and a frozen seed of a BL21(DE3)/pT7NS-CamAB strain were inoculated into a 15 mL test tube containing 3 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 37°C for 20 hours. 500 μL of the seed culture broth was inoculated into a 250 mL Erlenmeyer flask containing 50 mL of a L-broth medium (1.0% bactotripton, 0.5% yeast extract, 0.5% NaCl) containing 50 μg/mL of ampicillin and shake-cultured at 32°C for 4 hours. Then, 50 μL of 100 mM IPTG (isopropyl-β-D-thiogalactopyranoside) and 50 μL of 80 mg/mL 5-aminolevulinic acid were successively added thereto, and the medium was shake-cultured at 32°C for 5 hours. The obtained culture broth was centrifuged (5000 rpm, 10 minutes) to collect the mycelia. The mycelia were suspended in 1.75 mL of a 100 mM phosphate buffer solution (pH 6.1), and 250 μL of 80% glycerol and 12.5 μL of 40 mg/mL macrolide compound 11107B were added thereto. The conversion reaction solution obtained in this manner was reacted at 28°C for 24 hours. 400 μL of the reaction

solution was extracted with 600 μL of methanol and the extract was subjected to HPLC to measure each amount of macrolide compounds 11107B and 11107D. The results are shown in Table 7. Also, the details of the condition of HPLC are shown below.

Analyzer: Shimadzu HPLC 10Avp

Column: Develosil ODS UG-3 (φ4.6 mm × 250 mm 3 μm)

Mobile phase: 45% to 55% methanol (0 to 5 minutes)
55% methanol (5 to 13 minutes)
55% to 70% methanol (13 to 17 minutes)
70% methanol (17 to 21 minutes)
45% methanol (21 to 25 minutes)

Flow rate: 1.2 mL/min.

Detection: UV 240 nm

Injection capacity: 5 μL

Column temperature: 40°C

Analyzing time: 25 minutes

Retention time: 11107B 12.2 minutes
11107D 4.2 minutes

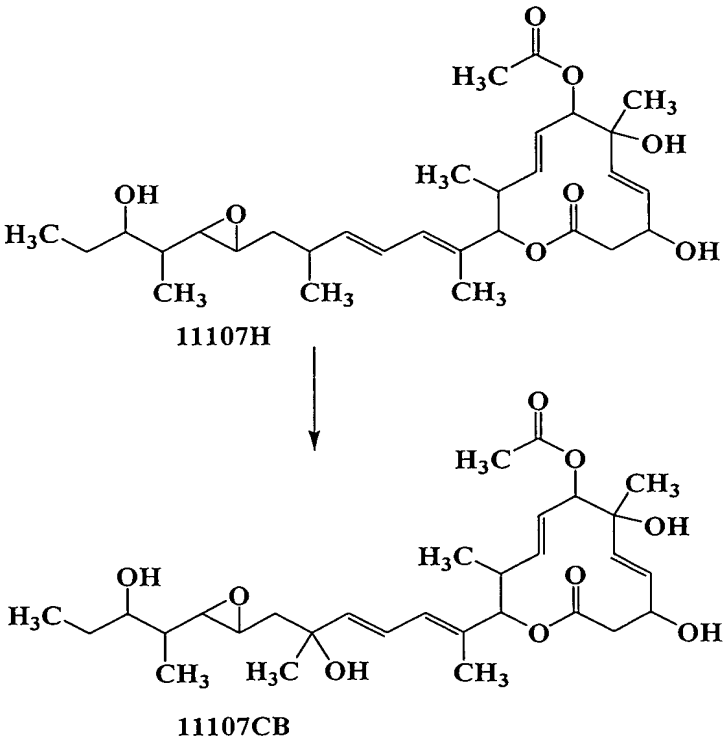
Table 7

mg/L	BL21(DE3)/pT7NS-CamAB	BL21(DE3)/pTC-tpmAB
11107B	141	128
11107D	0	18

As a result, the peak of the macrolide compound 11107D was not observed in the case of the E. coli BL21(DE3)/pT7NS-CamAB strain used as a control, whereas the peak of 11107D was obtained in the case of the BL21(DE3)/pTC-tpmAB strain containing the

tpmA and tpmB. This fact suggests that the tpmA and the tpmB participate in the conversion of 11107B into 11107D.

Example 13: Conversion of 11107H into 11107CB represented by the following formulae by a self-cloning strain



(1) Preparation of a transformant reaction solution

A medium containing 2.0% of Stabilose, 2.0% of glucose, 2.0% of a soybean meal (Honen Soypro), 0.5% of yeast extract and 0.32% of $CaCO_3$ and having a pH of 7.4 was prepared. A 250 mL Erlenmeyer flask was charged with 25 mL of the medium, which was then sterilized under heating at 121°C for 20 minutes and thiostrepton was added to the medium such that its final concentration was 25 mg/L. Then, 1% of an A-1544/pIJDMG strain from frozen seed was inoculated to culture the seed at 28°C and 220 rpm for 3 days. 1% of the seed culture broth was added in

a medium having the same composition to carry out main culturing at 28°C and 220 rpm for 2 days. After the main culturing was finished, mycelia were collected from the culture broth by centrifugation and suspended in 20 mL of phosphate buffer solution having a pH of 6.5. The substrate 11107H (100 g/L DMSO solution) was added in this mycelia suspended solution such that its final concentration was 2000 mg/L to run a conversion reaction at 28°C and 220 rpm for 16 hours.

(2) Isolation of a macrolide compound 11107CB from a transformant reaction solution

Mycelia were isolated from a conversion reaction solution (in an amount corresponding to 6 flasks) obtained from the same operation, by centrifugation and the centrifuged supernatant was extracted with the equal amount of ethyl acetate twice. The extract was concentrated and then the residue was purified by thin layer chromatography (MERCK Silicagel 60 F254' 0.5 mm, developing solution: toluene:acetone=1:1), to obtain 119.5 mg of 11107CB.

^{1}H-NMR spectrum (CD_3OD, 500MHz): δ ppm (integral, multiplicity, coupling constant J(Hz)):

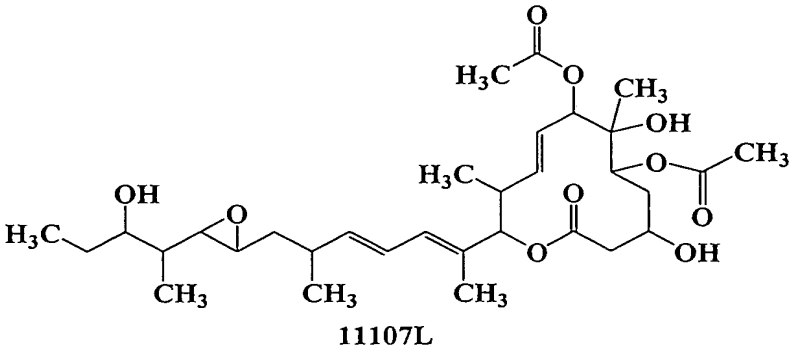
0.81(3H,d,J=6.7Hz), 0.89(3H,d,J=7.0), 0.94(3H,t,J=7.4Hz), 1.25(3H,s), 1.30-1.20(1H,m), 1.33(3H,s), 1.55-1.40(2H,m), 1.65(1H,dd,J=6.3,14.0Hz), 1.75(3H,s), 1.88(1H,dd,J=5.4,14.0Hz), 2.07(3H,s), 2.68-2.40(4H,m), 2.89(1H,m), 3.51(1H,m), 4.51(1H,m), 4.97(1H,d,J=8.6Hz), 4.99(1H,d,J=9.3Hz), 5.30(1H,dd,J=9.7,15.2Hz),

5.52(1H,dd,J=9.4,15.2Hz), 5.58(1H,dd,J=1.9,15.5Hz),

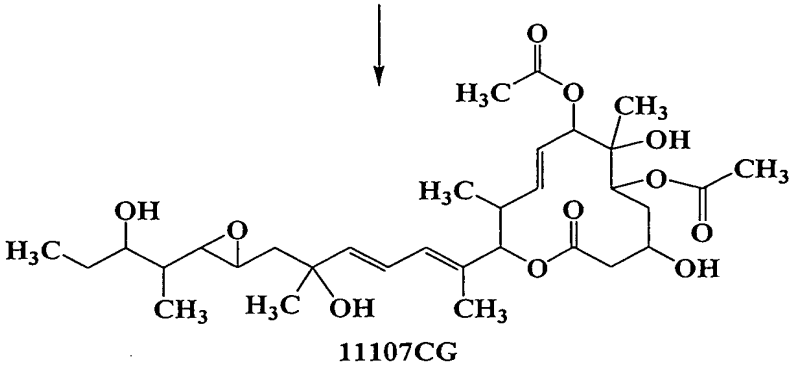
5.78(1H,dd,J=2.8,15.5Hz), 5.85(1H,d,J=15.3Hz),

6.07(1H,d,J=11.0Hz), 6.51(1H,dd,J=11.0,15.3Hz)

Example 14: Conversion of 11107L into 11107CG represented by the following formulae respectively by a self-cloning strain



11107L



11107CG

(1) Preparation of a transformant reaction solution

A medium containing 2.0% of stabilose, 2.0% of glucose, 2.0% of a soybean meal (Honen Soypro), 0.5% of yeast extract and 0.32% of $CaCO_3$ and having a pH of 7.4 was prepared. A 250 mL Erlenmeyer flask was charged with 25 mL of the medium, which was then sterilized under heating at 121°C for 20 minutes and thiostrepton was added to the medium such that its final concentration was 25 mg/L. Then, 1% of an A-1544/pIJDMG strain from frozen stock was inoculated to cultivate the seed culture

at 28°C and 220 rpm for 3 days. 1% of this seed culture broth was added in a medium having the same composition to carry out main cultivation at 28°C and 220 rpm for 2 days. After the main cultivation was finished, mycelia were collected from the culture broth by centrifugation and suspended in 20 mL of phosphate buffer solution having a pH of 6.5. The substrate 11107L (100 g/L DMSO solution) was added to this mycelia suspension solution such that its final concentration was 1600 mg/L to run a conversion reaction at 28°C and 220 rpm for 16 hours.

(2) Isolation of a macrolide compound 11107CG from a transformant reaction solution

Mycelia were isolated from the conversion reaction solution by centrifugation and the centrifuged supernatant was extracted with the equivalent amount of ethyl acetate twice. The extract layers were concentrated and then the residue was purified by thin layer chromatography (MERCK Silicagel 60 F254' 0.25 mm, developing solution: toluene:acetone=1:1), to obtain 25 mg of 11107CG.

ESI-MS m/z 633 $(M+Na)^+$

^{1}H-NMR spectrum (CD_3OD, 500MHz): δ ppm ((integral, multiplicity, coupling constant J (Hz)):

0.88(3H,d,J=6.7Hz), 0.90(3H,d,J=7.0Hz), 0.94(3H,d,J=7.4Hz), 1.18(3H,s), 1.30-1.20(1H,m), 1.34,(3H,s), 1.56-1.40(2H,m), 1.66(1H,dd,J=6.2,14.0Hz), 1.79-.169(2H,m), 1.81(3H,d,J=1.0Hz), 1.86(1H,dd,J=5.4,14.0Hz), 2.05(3H,s), 2.08(3H,s), 2.52(1H,dd,J=4.2,15.2Hz), 2.64-2.55(1H,m),

2.67(1H,dd,J=2.2,7.9Hz), 2.78(1H,dd,J=3.0,15.2Hz),
2.90(1H,dt,J=2.2,5.6Hz), 3.52(1H,dt,J=4.4,8.8Hz), 3.75(1H,m),
4.98(1H,dd,J=2.8,11.3Hz), 5.08(1H,d,J=9.7Hz),
5.13(1H,d,J=9.6Hz), 5.61(1H,dd,J=9.9,15.2Hz),
5.75(1H,dd,J=9.7,15.2Hz), 5.88(1H,d,J=15.3Hz),
6.13(1H,d,J=11.0Hz), 6.54(1H,dd,J=11.0,15.3Hz)

Industrial applicability

A 12-membered macrolide compound which has hydroxyl group at the 16-position and is exellent in antitumor activity and stability in an aqueous solution can be produced efficiently by using a transformant obtained by transformation using a plasmid carrying the DNA of the present invention.